



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 09:02 PM UTC

PDB ID : 8WI7 / pdb_00008wi7
EMDB ID : EMD-37559
Title : Cryo- EM structure of Mycobacterium smegmatis 70S ribosome, bS1 and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

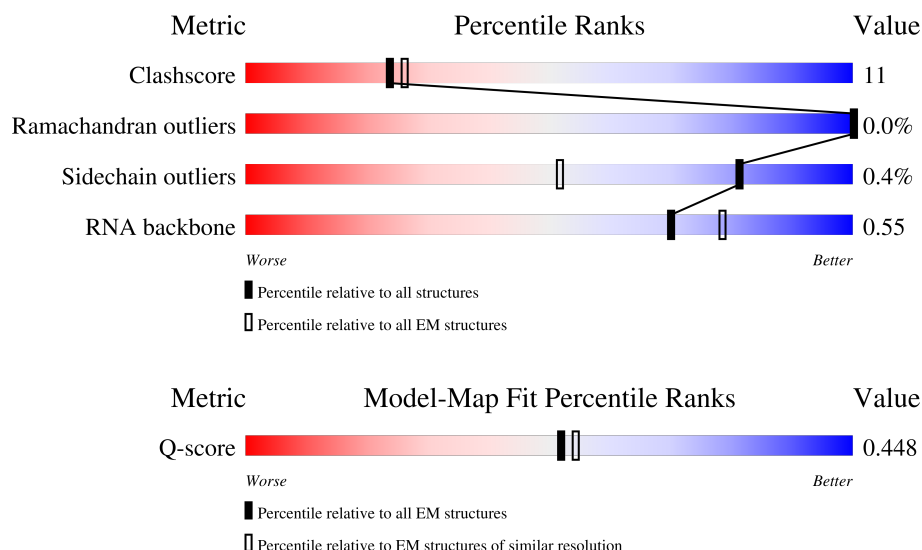
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	E	278	 81% 18% .
2	F	217	 84% 13% .
3	G	215	 84% 13% .

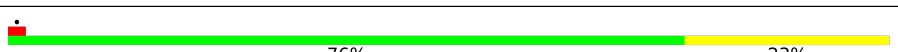
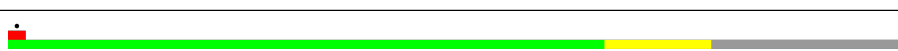
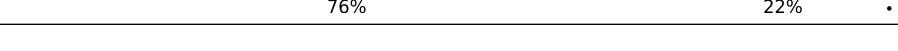
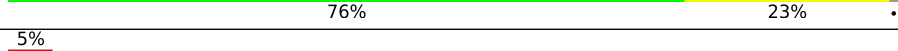
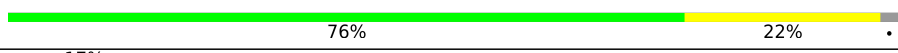
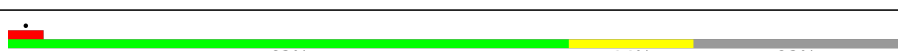
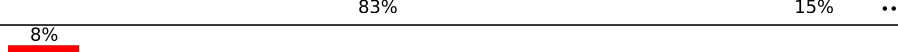
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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

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Mol	Chain	Length	Quality of chain
29	a	1528	
30	b	479	
31	v	33	
32	d	275	
33	e	201	
34	f	214	
35	g	96	
36	h	156	
37	i	132	
38	j	150	
39	k	101	
40	l	138	
41	m	124	
42	n	124	
43	o	101	
44	p	89	
45	q	156	
46	r	98	
47	s	84	
48	t	93	
49	u	86	
50	c	277	
51	w	264	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 144808 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	95	Total	C	N	O	0	0
			747	474	136	137		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	93	Total	C	N	O	S	0	0
			710	443	133	132	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	76	Total	C	N	O	0	0
			568	352	120	96		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	62	Total	C	N	O	0	0
			498	300	114	84		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	59	Total	C	N	O	S	0	0
			458	284	84	85	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3025	Total	C	N	O	P	0	0
			64965	28956	11946	21038	3025		

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 29 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	1515	Total	C	N	O	P	0	0
			32521	14485	5945	10576	1515		

- Molecule 30 is a protein called 30S ribosomal protein bS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	154	Total	C	N	O		0	0
			1193	758	198	237			

- Molecule 31 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	207	Total	C	N	O	S	0	0
			1656	1034	321	297	4		

- Molecule 33 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	168	Total	C	N	O	S	0	0
			1223	769	230	220	4		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 37 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 38 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	121	Total	C	N	O	S	0	0
			949	588	195	164	2		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 43 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 44 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 45 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 47 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	u	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 50 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	c	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 51 is a protein called Ribosome hibernation promotion factor RafH.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	255	Total	C	N	O	S	0	0
			2030	1273	387	364	6		

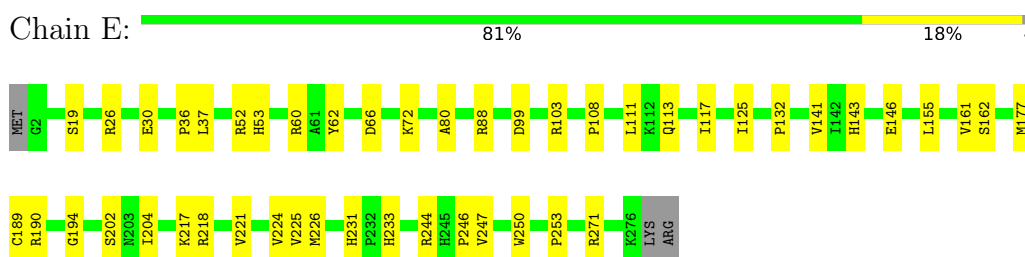
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

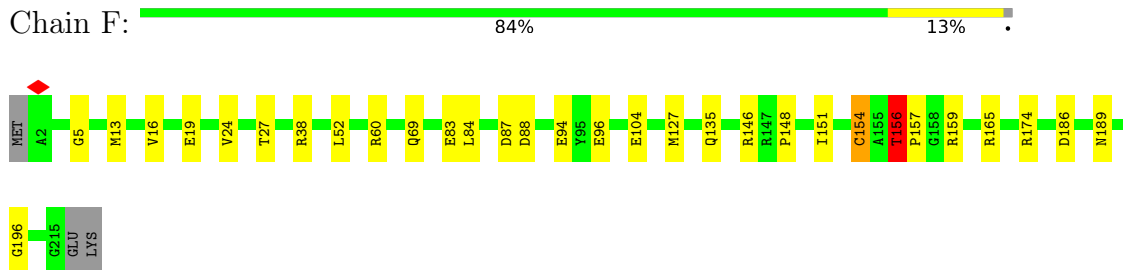
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

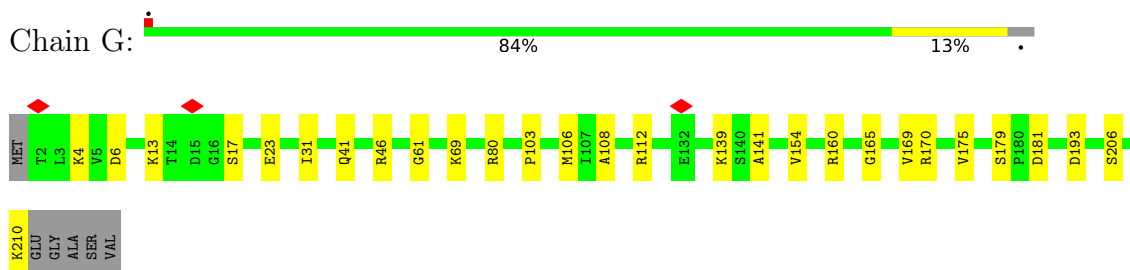
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

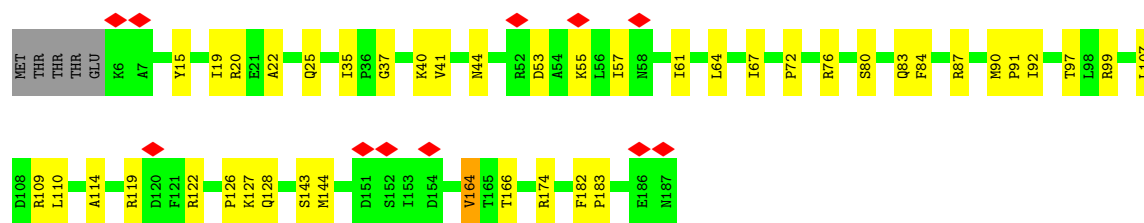


- Molecule 3: 50S ribosomal protein L4

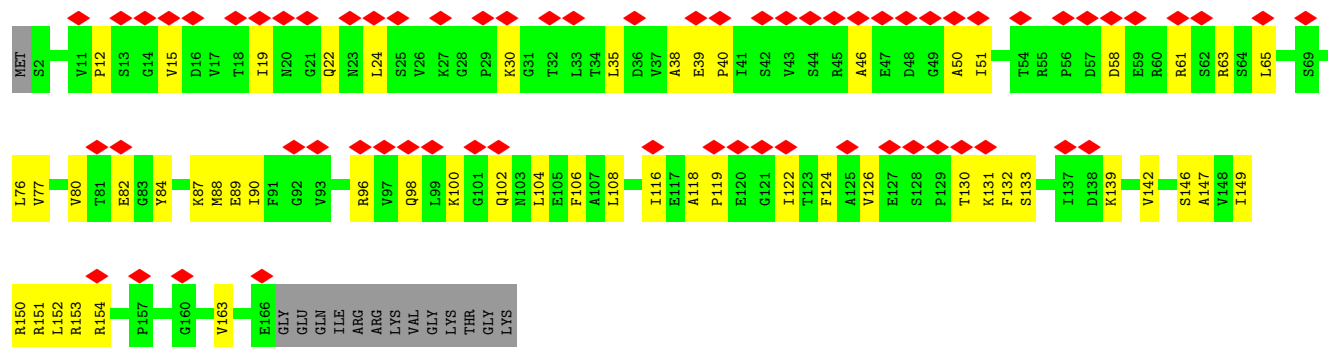


- Molecule 4: 50S ribosomal protein L5

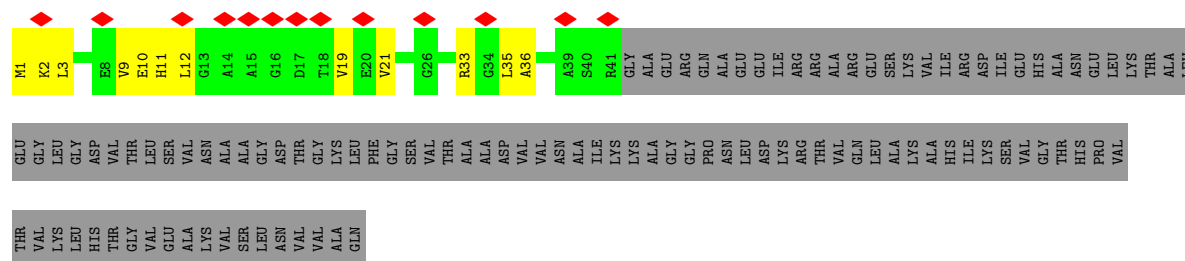




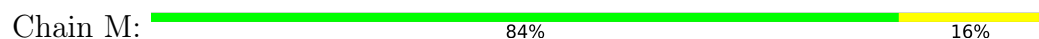
• Molecule 5: 50S ribosomal protein L6



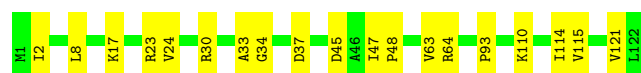
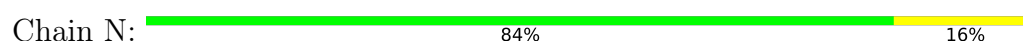
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L13

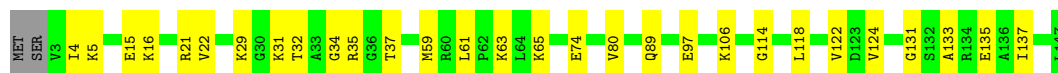


• Molecule 8: 50S ribosomal protein L14

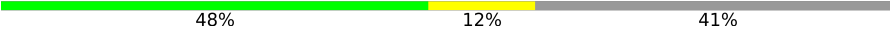


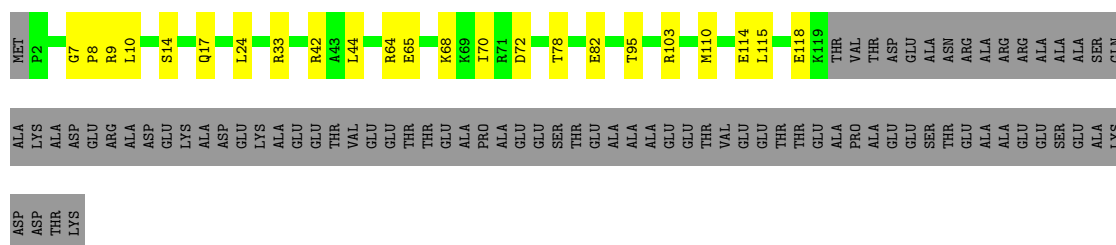
• Molecule 9: 50S ribosomal protein L15

Chain O:  79% 20% .



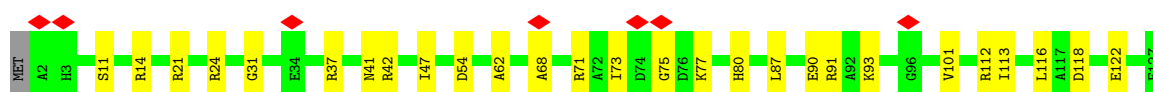
- Molecule 10: 50S ribosomal protein L17

Chain Q:  48% 12% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R:  6% 78% 21% .



- Molecule 12: 50S ribosomal protein L19

Chain S:  85% 15%



- Molecule 13: 50S ribosomal protein L20

Chain T:  80% 16%



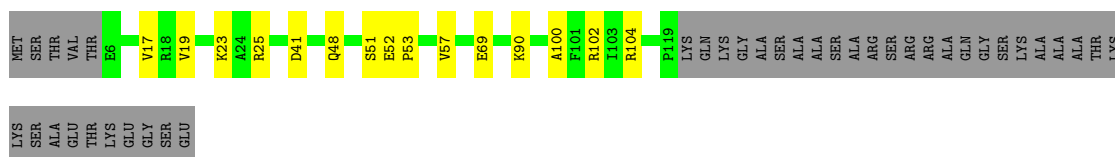
- Molecule 14: 50S ribosomal protein L21

Chain U:  82% 16%



- Molecule 15: 50S ribosomal protein L22

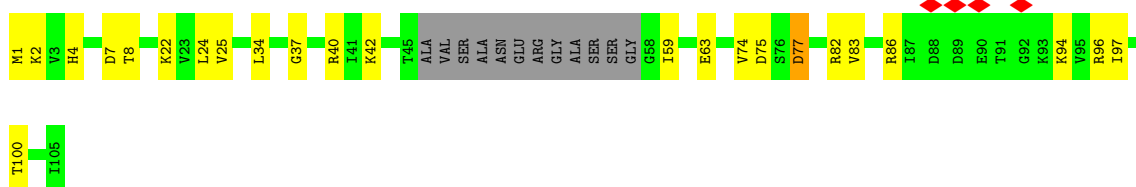
Chain V:  65% 10% 25%



- Molecule 16: 50S ribosomal protein L23



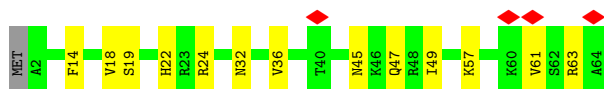
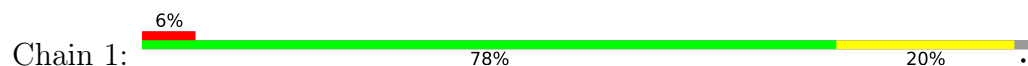
- Molecule 17: 50S ribosomal protein L24



- Molecule 18: 50S ribosomal protein L27



- Molecule 19: 50S ribosomal protein L28



- Molecule 20: 50S ribosomal protein L29

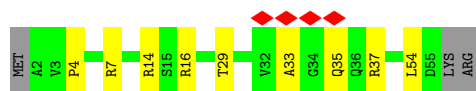
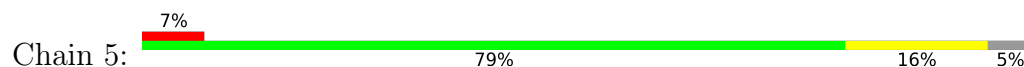


- Molecule 21: 50S ribosomal protein L30

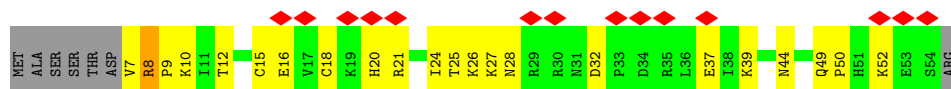




- Molecule 22: 50S ribosomal protein L32



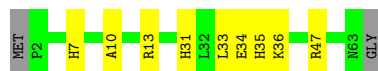
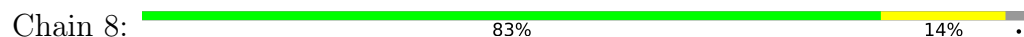
- Molecule 23: 50S ribosomal protein L33A



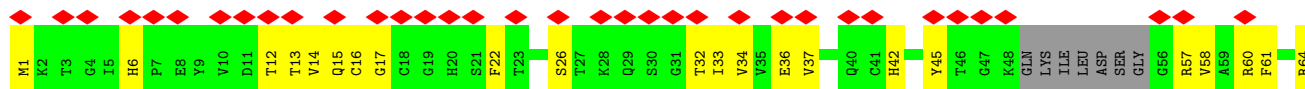
- Molecule 24: 50S ribosomal protein L34



- Molecule 25: 50S ribosomal protein L35



- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 23S rRNA



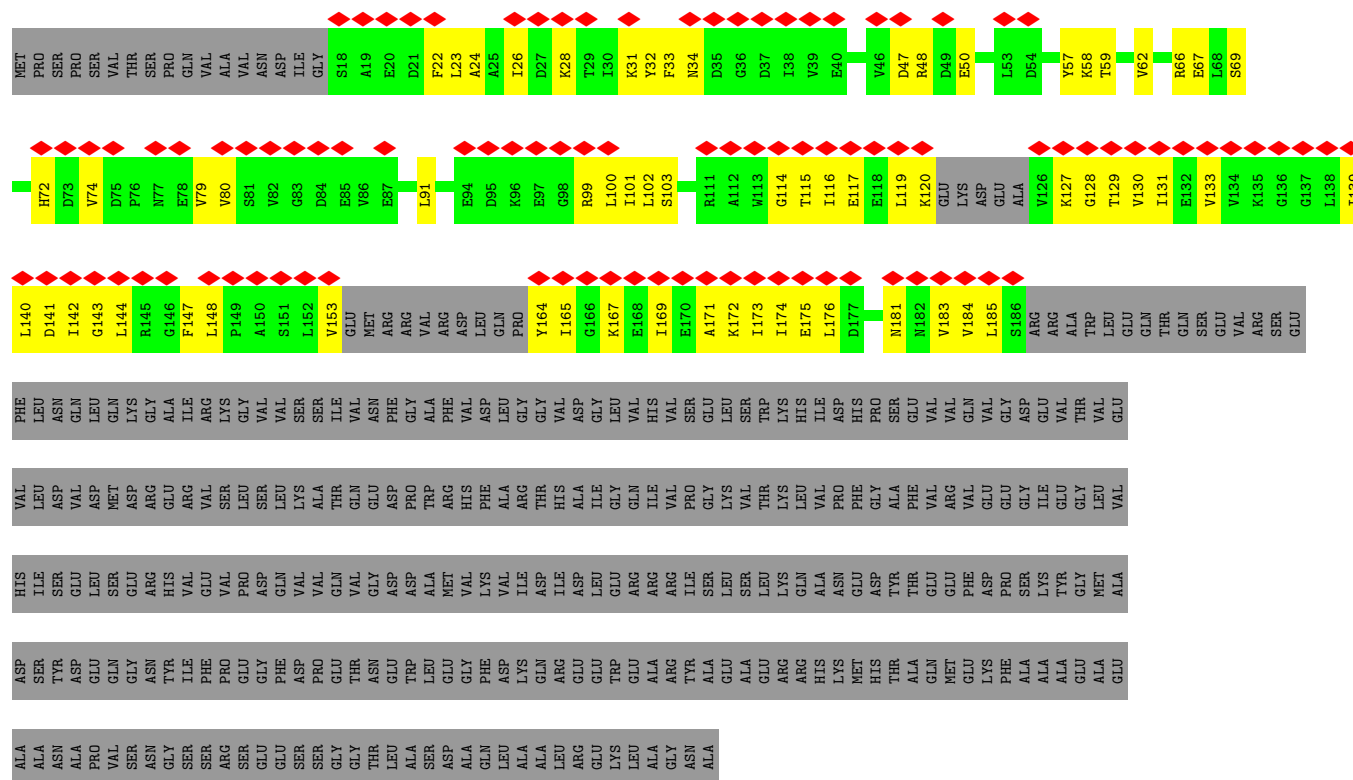
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U	G1156	A1075	G996	A909	G815	A727	G645	G551	U453	U367	G299	G219	A116
C	G1157	A1076	G997	U911	U818	G728	G646	G554	U454	G369	U301	A221	U117
A	G1158	A1077	G998	C912	G819	G730	G647	G555	G460	U370	U302	A222	U122
G	C1161	G1078	C999	A919	G824	A731	G650	G556	A465	G371	U303	A223	A122
G	G1162	U1084	C1000	G920	G825	G732	G653	G557	G470	C377	U304	A227	C125
A	A1163	G1085	C1001	G921	G826	U733	U654	U563	C471	G378	G305	U229	C130
G	A1164	C1086	C1002	G924	G827	U735	G655	G564	G472	G379	U306	G230	A131
G	G1165	G1087	A1003	G925	G828	G736	C656	G565	C473	A380	G307	U231	C132
G	A1166	U1088	C1004	C927	G829	A737	U656	A566	C474	A381	G308	U234	G137
C	G1090	C1089	C1005	U928	U829	A738	U657	A567	U475	U383	G309	U235	A138
U	A1006	G1090	A1006	C929	A830	U739	U658	A568	G476	G384	G310	U139	U139
G	G1092	A1091	G1007	C932	G831	A740	U661	G569	U479	G385	G311	U239	G140
A	A1099	G1092	G832	C933	G833	G741	G662	U586	A479	U388	G312	G242	A148
G	C1100	A1099	G833	U942	U839	G742	G663	G587	U480	G389	G313	G242	G149
G	A1101	C1100	A1010	A935	U840	G743	A664	A588	U481	U316	G314	G242	C149
U	A1106	G1107	U1010	A936	G841	A747	A665	A589	U482	U317	U315	G248	C150
U	G1107	A1106	C1011	U943	G842	U748	A666	A590	G483	A392	U318	C249	A151
G	C1110	C1110	C1012	G945	G844	C749	A667	A591	G484	A393	U319	G250	G152
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G	A1118	C1020	G952	U954	U858	A755	U675	U598	U490	U403	U330	G263	A164
A	A1119	A1020	U954	U954	U859	A756	G676	G599	G491	A404	U331	G264	U165
A	G1120	G1021	G960	G960	U860	A757	U677	A600	G499	A405	G334	G265	G176
C	G1121	C1022	U961	U961	G861	G758	G678	A601	C502	A412	G335	U270	G183
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A	A1139	U1044	G977	G977	U871	G768	G688	C513	A512	A430	U345	C281	A198
A	G1140	A1047	A978	A978	U872	G769	G689	C514	A513	A431	U346	U282	A199
A	A1141	U1048	G979	G979	U873	G770	G690	C515	A514	A432	U347	U283	U204
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G	A1145	U1052	A987	A987	U877	G774	G694	C519	A518	A436	U351	U287	G204
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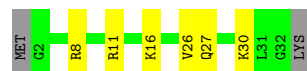
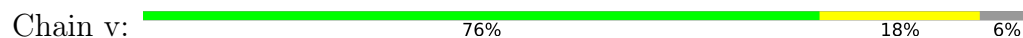




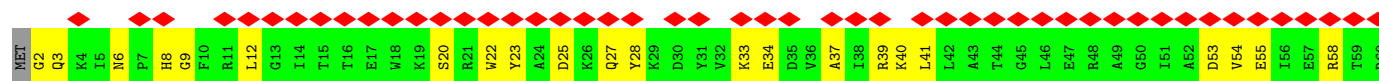
- Molecule 30: 30S ribosomal protein bS1

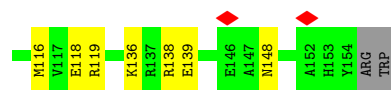


- Molecule 31: 30S ribosomal protein S22



- Molecule 32: 30S ribosomal protein S3





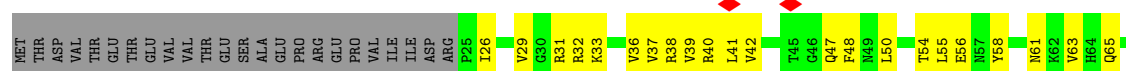
- Molecule 37: 30S ribosomal protein S8

Chain i: 76% 23%



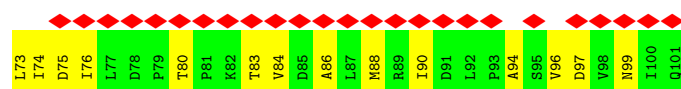
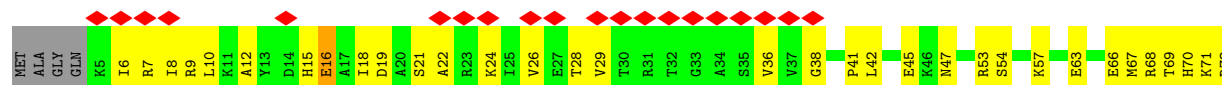
- Molecule 38: 30S ribosomal protein S9

Chain j: 5% 50% 34% 16%



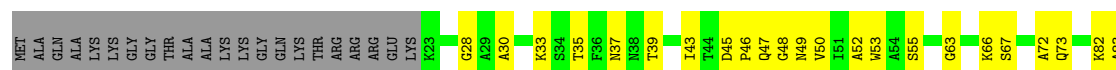
- Molecule 39: 30S ribosomal protein S10

Chain k: 45% 50% 46%



- Molecule 40: 30S ribosomal protein S11

Chain l: 50% 33% 17%

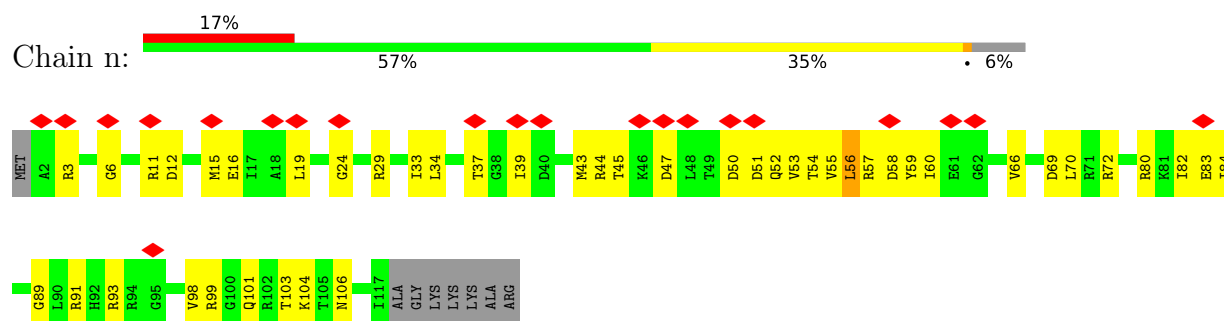


- Molecule 41: 30S ribosomal protein S12

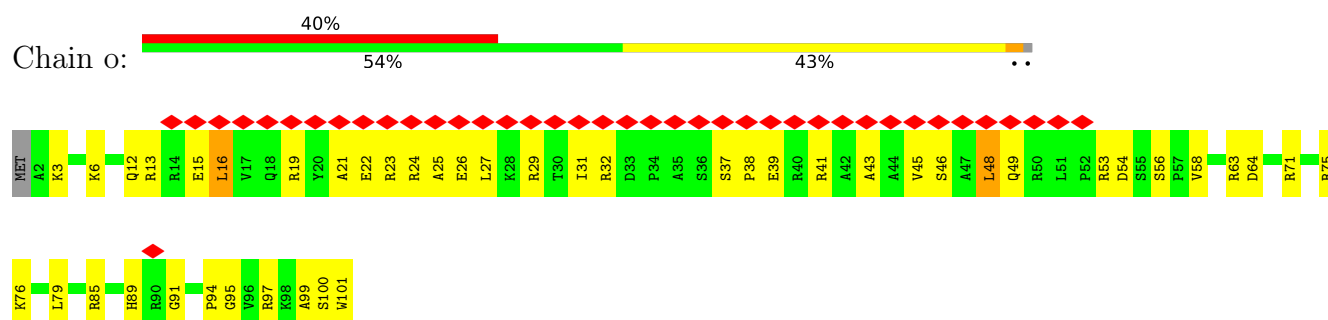
Chain m: 76% 22%



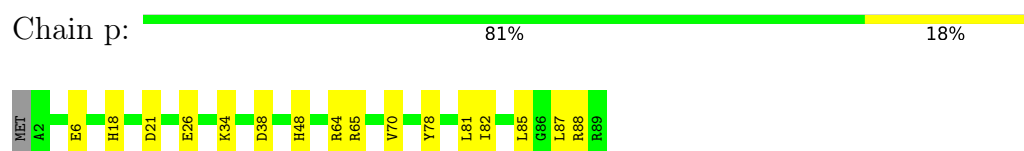
- Molecule 42: 30S ribosomal protein S13



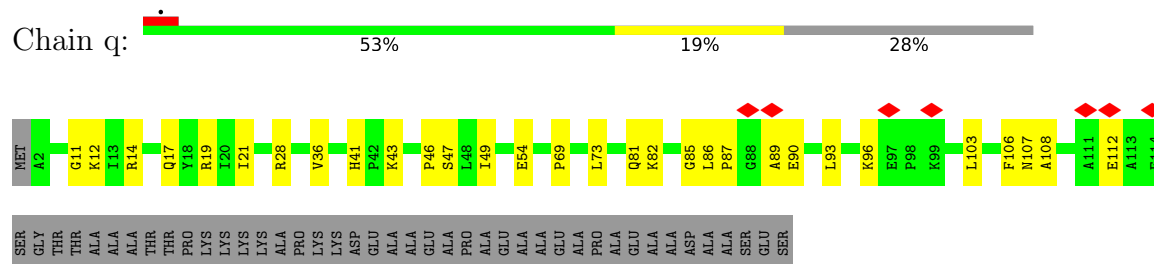
- Molecule 43: 30S ribosomal protein S14A



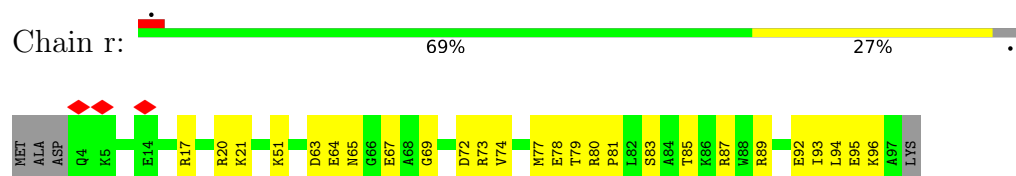
- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16

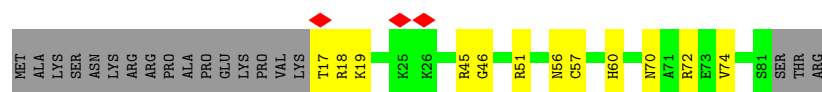


- Molecule 46: 30S ribosomal protein S17

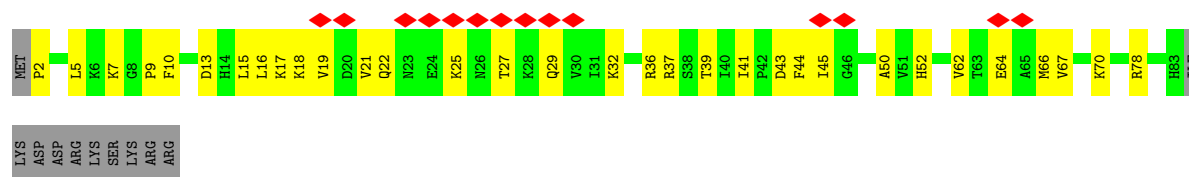


- Molecule 47: 30S ribosomal protein S18B

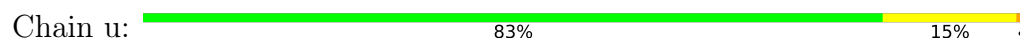




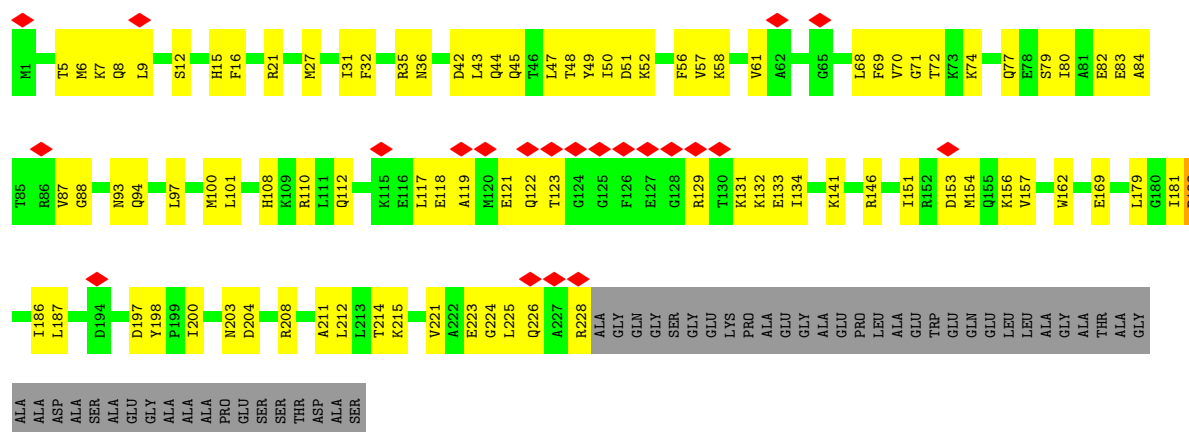
• Molecule 48: 30S ribosomal protein S19



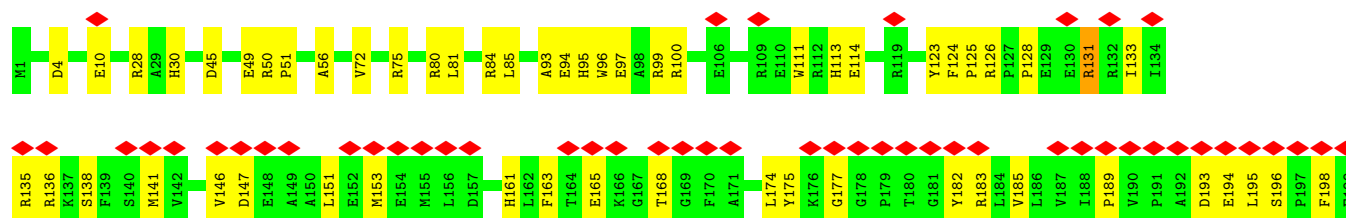
• Molecule 49: 30S ribosomal protein S20

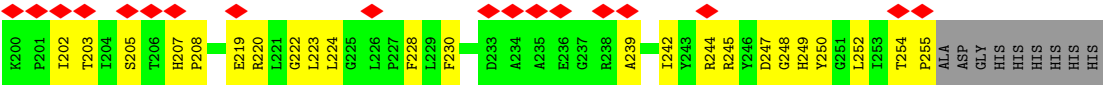


• Molecule 50: 30S ribosomal protein S2



• Molecule 51: Ribosome hibernation promotion factor Rahf





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.212	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	E	0.13	0/2153	0.27	0/2895
2	F	0.17	0/1609	0.41	0/2165
3	G	0.12	0/1592	0.27	0/2153
4	H	0.13	0/1467	0.35	0/1973
5	I	0.13	0/1281	0.35	0/1733
6	J	0.22	0/311	0.46	0/419
7	M	0.14	0/1157	0.32	0/1567
8	N	0.13	0/946	0.29	0/1268
9	O	0.13	0/1091	0.37	0/1457
10	Q	0.13	0/945	0.30	0/1267
11	R	0.15	0/966	0.43	0/1298
12	S	0.15	0/921	0.34	0/1236
13	T	0.14	0/1000	0.29	0/1341
14	U	0.15	0/764	0.30	0/1030
15	V	0.13	0/887	0.30	0/1204
16	W	0.15	0/757	0.33	0/1018
17	X	0.14	0/716	0.35	0/957
18	Z	0.15	0/577	0.31	0/774
19	1	0.12	0/478	0.30	0/641
20	2	0.13	0/534	0.32	0/713
21	3	0.15	0/477	0.32	0/640
22	5	0.13	0/427	0.28	0/572
23	6	0.19	0/405	0.47	0/542
24	7	0.11	0/380	0.29	0/500
25	8	0.10	0/503	0.27	0/667
26	4	0.15	0/467	0.36	0/626
27	A	0.12	0/72743	0.26	0/113499
28	B	0.11	0/2821	0.24	0/4396
29	a	0.12	0/36400	0.27	1/56798 (0.0%)
30	b	0.16	0/1201	0.48	0/1615
31	v	0.11	0/271	0.25	0/348
32	d	0.15	0/1680	0.37	1/2256 (0.0%)
33	e	0.12	0/1672	0.29	0/2251
34	f	0.13	0/1239	0.29	0/1673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.14	0/782	0.36	0/1059
36	h	0.13	0/1225	0.36	1/1653 (0.1%)
37	i	0.13	0/1025	0.29	0/1385
38	j	0.16	0/1012	0.41	0/1362
39	k	0.23	0/789	0.49	0/1069
40	l	0.16	0/873	0.38	0/1180
41	m	0.13	0/960	0.31	0/1283
42	n	0.14	0/942	0.40	0/1260
43	o	0.26	0/830	0.45	0/1106
44	p	0.14	0/729	0.32	0/977
45	q	0.14	0/908	0.36	0/1226
46	r	0.12	0/759	0.32	0/1016
47	s	0.12	0/518	0.28	0/693
48	t	0.14	0/680	0.37	0/915
49	u	0.16	0/663	0.40	0/882
50	c	0.14	0/1822	0.40	1/2457 (0.0%)
51	w	0.14	0/2078	0.33	0/2816
All	All	0.13	0/157433	0.29	4/235831 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	c	182	PRO	CA-N-CD	-8.06	100.71	112.00
36	h	58	PRO	CA-N-CD	-8.04	100.74	112.00
32	d	108	PRO	CA-N-CD	-6.88	102.36	112.00
29	a	1425	G	C4'-C3'-O3'	-5.11	105.34	113.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1587	0	1630	28	0
3	G	1569	0	1607	21	0
4	H	1445	0	1476	43	0
5	I	1260	0	1300	41	0
6	J	308	0	323	10	0
7	M	1130	0	1167	25	0
8	N	938	0	1000	15	0
9	O	1078	0	1151	25	0
10	Q	928	0	972	14	0
11	R	956	0	991	22	0
12	S	907	0	938	22	0
13	T	988	0	1038	22	0
14	U	754	0	802	11	0
15	V	873	0	909	12	0
16	W	747	0	794	7	0
17	X	710	0	760	18	0
18	Z	568	0	586	11	0
19	1	470	0	484	11	0
20	2	531	0	541	12	0
21	3	474	0	500	12	0
22	5	423	0	463	9	0
23	6	397	0	407	20	0
24	7	377	0	411	17	0
25	8	498	0	538	7	0
26	4	458	0	447	92	0
27	A	64965	0	32687	1010	0
28	B	2522	0	1285	40	0
29	a	32521	0	16366	603	0
30	b	1193	0	1238	46	0
31	v	271	0	329	7	0
32	d	1656	0	1704	62	0
33	e	1641	0	1668	36	0
34	f	1223	0	1287	25	0
35	g	771	0	797	47	0
36	h	1207	0	1259	25	0
37	i	1010	0	1046	23	0
38	j	994	0	1050	55	0
39	k	775	0	808	54	0
40	l	855	0	863	40	0
41	m	949	0	1032	21	0
42	n	935	0	985	109	0
43	o	819	0	866	84	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	p	720	0	760	14	0
45	q	891	0	935	28	0
46	r	748	0	795	20	0
47	s	513	0	540	9	0
48	t	662	0	677	41	0
49	u	660	0	712	11	0
50	c	1793	0	1839	66	0
51	w	2030	0	2023	86	0
All	All	144808	0	96951	2581	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (2581) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:37:VAL:HB	42:n:57:ARG:CZ	1.41	1.51
26:4:37:VAL:HB	42:n:57:ARG:NH1	1.19	1.46
26:4:36:GLU:C	42:n:57:ARG:HH22	1.23	1.46
26:4:37:VAL:N	42:n:57:ARG:HH22	1.16	1.42
27:A:1611:A:H2	35:g:17:ARG:NH2	1.22	1.34
26:4:36:GLU:CD	42:n:53:VAL:HB	1.08	1.33
26:4:36:GLU:CD	42:n:53:VAL:CB	1.88	1.27
26:4:36:GLU:CG	42:n:53:VAL:HB	1.64	1.26
27:A:1611:A:C2	35:g:17:ARG:NH2	2.03	1.26
26:4:37:VAL:N	42:n:57:ARG:NH2	1.83	1.25
32:d:28:TYR:OH	43:o:94:PRO:HD2	1.36	1.24
26:4:60:ARG:CZ	29:a:1293:G:OP1	1.83	1.24
26:4:37:VAL:CB	42:n:57:ARG:NH1	2.01	1.24
27:A:1560:U:O2	35:g:17:ARG:CZ	1.87	1.23
29:a:1290:C:P	42:n:101:GLN:HE22	1.62	1.23
4:H:122:ARG:HD2	42:n:72:ARG:NH2	1.53	1.21
26:4:36:GLU:OE2	42:n:50:ASP:O	1.53	1.21
27:A:2137:A:C2	29:a:1477:A:C5	2.28	1.20
4:H:143:SER:OG	42:n:3:ARG:NH2	1.71	1.19
51:w:124:PHE:CD2	51:w:126:ARG:HG2	1.76	1.19
29:a:598:C:O2	45:q:12:LYS:NZ	1.75	1.17
26:4:64:ARG:NH1	29:a:1294:G:OP2	1.77	1.17
27:A:1560:U:C1'	35:g:17:ARG:HD3	1.75	1.16
27:A:1560:U:O2	35:g:17:ARG:NE	1.79	1.15
39:k:68:ARG:NH2	43:o:97:ARG:HH21	1.44	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:57:ARG:HG2	48:t:67:VAL:O	1.47	1.14
29:a:1232:A:H62	29:a:1268:C:N4	1.44	1.14
27:A:2971:G:H21	27:A:2981:A:N6	1.45	1.14
26:4:36:GLU:C	42:n:57:ARG:NH2	2.05	1.12
29:a:1232:A:N6	29:a:1268:C:H42	1.46	1.12
26:4:36:GLU:CB	42:n:57:ARG:NH2	2.13	1.11
27:A:1560:U:C2'	35:g:17:ARG:HH11	1.62	1.11
26:4:36:GLU:OE2	42:n:53:VAL:CB	1.98	1.10
27:A:1560:U:H2'	35:g:17:ARG:HH11	1.13	1.10
12:S:38:ARG:NH1	29:a:345:C:H5'	1.68	1.09
29:a:1303:U:O2'	48:t:78:ARG:NH2	1.85	1.08
27:A:1560:U:H2'	35:g:17:ARG:NH1	1.70	1.06
26:4:60:ARG:NH2	29:a:1293:G:OP1	1.88	1.06
26:4:36:GLU:CD	42:n:50:ASP:O	1.97	1.06
27:A:2971:G:N2	27:A:2981:A:H62	1.52	1.06
32:d:28:TYR:OH	43:o:94:PRO:CD	2.04	1.06
27:A:1560:U:H1'	35:g:17:ARG:CD	1.86	1.04
26:4:36:GLU:OE2	42:n:53:VAL:N	1.91	1.03
29:a:1168:G:P	38:j:135:LYS:HE3	1.99	1.01
27:A:1560:U:H1'	35:g:17:ARG:HD3	1.02	1.01
29:a:1040:U:OP1	43:o:85:ARG:NH2	1.93	1.01
26:4:36:GLU:OE2	42:n:53:VAL:HB	1.59	1.00
29:a:1291:G:C8	42:n:99:ARG:NH2	2.29	1.00
29:a:1099:C:OP2	38:j:31:ARG:NH2	1.94	1.00
25:8:47:ARG:NH2	27:A:724:G:OP1	1.95	1.00
27:A:1610:C:H2'	27:A:1611:A:C8	1.96	1.00
26:4:37:VAL:CB	42:n:57:ARG:CZ	2.34	0.99
26:4:60:ARG:NH2	29:a:1293:G:C5'	2.25	0.99
26:4:60:ARG:HH22	29:a:1293:G:C5'	1.76	0.98
26:4:36:GLU:HB2	42:n:57:ARG:HH21	1.24	0.98
29:a:1168:G:OP1	38:j:135:LYS:HE3	1.62	0.98
26:4:57:ARG:CG	48:t:67:VAL:O	2.11	0.97
39:k:68:ARG:NH2	43:o:97:ARG:NH2	2.12	0.97
26:4:36:GLU:OE2	42:n:53:VAL:CA	2.13	0.96
27:A:1547:G:H1	27:A:1623:U:H3	1.01	0.96
27:A:1550:G:H1	27:A:1620:U:H3	1.13	0.95
51:w:124:PHE:HD2	51:w:126:ARG:HG2	1.14	0.95
26:4:60:ARG:NH2	29:a:1293:G:H5''	1.82	0.95
51:w:126:ARG:HG3	51:w:247:ASP:O	1.65	0.95
39:k:63:GLU:OE1	43:o:85:ARG:NH1	1.98	0.94
32:d:12:LEU:HD22	43:o:91:GLY:HA3	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:12:A:C6	33:e:201:LYS:HG3	2.03	0.94
4:H:143:SER:HB2	42:n:3:ARG:HH12	1.30	0.93
27:A:2137:A:O4'	51:w:75:ARG:NH2	2.00	0.93
29:a:1291:G:N7	42:n:99:ARG:NH2	2.13	0.93
29:a:1290:C:P	42:n:101:GLN:NE2	2.42	0.93
29:a:1171:G:OP1	32:d:3:GLN:O	1.86	0.92
27:A:1561:C:O4'	35:g:17:ARG:NH1	2.02	0.92
27:A:1562:C:H42	27:A:1608:U:H3	0.97	0.92
32:d:28:TYR:HH	43:o:94:PRO:HD2	1.13	0.92
27:A:1560:U:O2	35:g:17:ARG:CD	2.18	0.92
27:A:334:G:H1	27:A:347:U:H3	1.09	0.92
29:a:82:U:H3	29:a:87:G:H1	0.92	0.91
26:4:60:ARG:NH1	29:a:1293:G:OP1	2.03	0.91
19:1:57:LYS:NZ	27:A:488:G:N7	2.18	0.91
27:A:2971:G:H21	27:A:2981:A:H62	0.95	0.91
12:S:38:ARG:HD3	29:a:345:C:OP2	1.70	0.90
27:A:1559:A:H2'	27:A:1560:U:H6	1.34	0.90
4:H:122:ARG:HD2	42:n:72:ARG:CZ	2.01	0.90
27:A:2137:A:C2	29:a:1477:A:C4	2.59	0.90
4:H:143:SER:HG	42:n:3:ARG:HH22	1.15	0.90
4:H:143:SER:CB	42:n:3:ARG:HH12	1.86	0.88
27:A:2137:A:H2	29:a:1477:A:C5	1.92	0.88
12:S:105:LYS:HZ3	29:a:1448:G:P	1.96	0.88
29:a:949:C:H4'	38:j:147:TYR:CE1	2.09	0.87
29:a:1298:G:P	43:o:29:ARG:HH12	1.98	0.86
39:k:68:ARG:CZ	43:o:97:ARG:HH21	1.89	0.86
29:a:241:C:H5''	41:m:13:ARG:HH22	1.41	0.86
29:a:666:U:H1'	40:l:53:TRP:HE1	1.38	0.86
27:A:1540:U:H3	27:A:1632:G:H1	1.22	0.86
29:a:728:A:O2'	29:a:729:A:N7	2.07	0.86
38:j:133:ARG:HG3	43:o:101:TRP:NE1	1.91	0.86
27:A:2137:A:H2	29:a:1477:A:C4	1.92	0.85
26:4:36:GLU:HB3	42:n:57:ARG:NH2	1.90	0.85
32:d:12:LEU:CD2	43:o:91:GLY:HA3	2.07	0.85
27:A:2086:U:H3	27:A:2096:G:H1	0.85	0.85
39:k:63:GLU:CD	43:o:85:ARG:NH1	2.36	0.84
26:4:60:ARG:HH22	29:a:1293:G:H5'	1.42	0.84
27:A:1003:A:H62	42:n:93:ARG:HD2	1.41	0.84
29:a:83:U:O2	29:a:86:G:O6	1.96	0.84
29:a:745:G:H1	29:a:792:G:HO2'	1.25	0.84
40:l:121:ASP:HB2	51:w:223:LEU:HD11	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1342:A:N7	43:o:58:VAL:HG23	1.92	0.84
27:A:1559:A:H2'	27:A:1560:U:C6	2.13	0.83
26:4:36:GLU:HG3	42:n:53:VAL:HB	1.59	0.83
43:o:6:LYS:HB3	43:o:63:ARG:HH12	1.43	0.83
47:s:45:ARG:NH1	51:w:219:GLU:OE2	2.12	0.83
30:b:128:GLY:HA3	30:b:142:ILE:HG22	1.61	0.82
29:a:1290:C:H5''	42:n:98:VAL:HG22	1.60	0.82
29:a:1299:C:H4'	43:o:48:LEU:CD2	2.09	0.82
27:A:337:U:H3	27:A:344:G:H1	0.83	0.82
27:A:1609:G:H2'	27:A:1610:C:C6	2.14	0.82
6:J:10:GLU:OE2	6:J:11:HIS:ND1	2.13	0.82
29:a:1291:G:OP2	42:n:99:ARG:NE	2.10	0.81
29:a:644:G:H22	29:a:721:G:H1	1.28	0.81
29:a:956:A:C4	43:o:71:ARG:NH1	2.48	0.81
33:e:197:GLU:OE2	34:f:130:VAL:N	2.14	0.81
26:4:37:VAL:HB	42:n:57:ARG:HH12	1.46	0.81
39:k:68:ARG:HH22	43:o:97:ARG:NH2	1.79	0.81
51:w:124:PHE:HD2	51:w:126:ARG:CG	1.93	0.81
29:a:770:A:OP1	51:w:30:HIS:ND1	2.13	0.81
27:A:2137:A:C1'	51:w:75:ARG:NH2	2.43	0.80
27:A:2137:A:C1'	51:w:75:ARG:HH22	1.94	0.80
29:a:1299:C:H4'	43:o:48:LEU:HD21	1.64	0.80
12:S:38:ARG:HH11	29:a:345:C:H5'	1.47	0.80
10:Q:42:ARG:NH2	27:A:3038:C:OP1	2.15	0.79
51:w:128:PRO:HA	51:w:131:ARG:HG3	1.65	0.78
12:S:105:LYS:NZ	29:a:1448:G:P	2.57	0.78
40:l:118:THR:HA	51:w:220:ARG:NH2	1.99	0.77
26:4:36:GLU:CA	42:n:57:ARG:NH2	2.47	0.77
2:F:156:THR:HB	2:F:157:PRO:CD	2.15	0.77
26:4:60:ARG:NH2	29:a:1293:G:P	2.57	0.77
27:A:1754:G:N2	27:A:1759:A:N1	2.33	0.77
51:w:124:PHE:CD2	51:w:126:ARG:CG	2.62	0.77
29:a:1172:A:OP1	32:d:3:GLN:HB3	1.84	0.77
26:4:36:GLU:CB	42:n:57:ARG:HH21	1.83	0.77
27:A:1560:U:O2	35:g:17:ARG:HD3	1.85	0.77
26:4:60:ARG:HH22	29:a:1293:G:P	2.07	0.77
12:S:38:ARG:NH1	29:a:345:C:C5'	2.46	0.77
29:a:1159:G:OP1	38:j:115:ARG:NH1	2.19	0.76
29:a:1443:G:OP1	49:u:26:SER:OG	2.03	0.76
29:a:1476:A:O2'	51:w:80:ARG:NH2	2.18	0.76
29:a:149:A:N6	29:a:166:C:O2	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1298:G:P	43:o:29:ARG:NH1	2.58	0.76
27:A:2137:A:C2	29:a:1477:A:C6	2.73	0.75
27:A:747:A:N6	27:A:768:G:O2'	2.19	0.75
29:a:241:C:H5''	41:m:13:ARG:NH2	2.02	0.75
27:A:1533:U:OP2	27:A:1535:C:N4	2.18	0.75
29:a:936:G:H21	29:a:1208:A:H62	1.34	0.75
2:F:156:THR:HB	2:F:157:PRO:HD2	1.68	0.75
26:4:60:ARG:HH21	29:a:1293:G:H5''	1.47	0.75
29:a:1338:G:H2'	29:a:1339:A:H8	1.52	0.75
39:k:67:MET:HG3	43:o:95:GLY:O	1.87	0.75
10:Q:103:ARG:HD3	10:Q:110:MET:HE2	1.67	0.75
29:a:1133:G:OP1	39:k:70:HIS:ND1	2.14	0.75
27:A:2333:G:O2'	27:A:2343:G:OP2	2.04	0.75
29:a:826:U:H4'	47:s:19:LYS:HE2	1.69	0.75
46:r:64:GLU:OE1	46:r:64:GLU:N	2.19	0.75
29:a:606:U:P	45:q:19:ARG:HH21	2.09	0.74
27:A:1003:A:N6	42:n:93:ARG:HD2	2.02	0.74
4:H:143:SER:OG	42:n:3:ARG:CZ	2.34	0.74
30:b:66:ARG:HH22	30:b:72:HIS:HA	1.50	0.74
32:d:86:ILE:HD13	32:d:100:LEU:HD13	1.67	0.74
38:j:37:VAL:HG22	38:j:87:LEU:HD22	1.70	0.74
51:w:124:PHE:HE2	51:w:126:ARG:CD	2.00	0.74
27:A:279:U:H3	27:A:307:G:H1	1.35	0.74
51:w:124:PHE:CE2	51:w:126:ARG:HG2	2.23	0.74
2:F:148:PRO:O	27:A:2735:U:O2'	2.06	0.74
13:T:25:ARG:NH1	27:A:2245:C:OP1	2.21	0.73
29:a:1342:A:C5	43:o:58:VAL:HG23	2.23	0.73
32:d:23:TYR:CZ	39:k:97:ASP:HB3	2.22	0.73
32:d:62:ARG:HH12	32:d:64:ARG:HB2	1.52	0.73
43:o:49:GLN:OE1	48:t:10:PHE:CE1	2.42	0.73
26:4:37:VAL:CB	42:n:57:ARG:HH12	1.96	0.73
27:A:217:G:H22	27:A:235:U:H4'	1.53	0.73
29:a:772:A:O2'	29:a:774:A:N7	2.20	0.73
29:a:1221:U:N3	36:h:32:LEU:HD12	2.03	0.73
26:4:37:VAL:CG2	42:n:57:ARG:NH1	2.51	0.73
29:a:965:A:OP1	43:o:6:LYS:NZ	2.20	0.73
30:b:120:LYS:HZ2	30:b:176:LEU:HD22	1.54	0.73
27:A:2386:U:OP1	27:A:2393:A:O2'	2.05	0.73
3:G:41:GLN:HG2	27:A:709:U:H1'	1.69	0.72
27:A:1996:U:OP2	27:A:2001:A:N6	2.19	0.72
27:A:1560:U:O2	35:g:17:ARG:NH1	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:d:28:TYR:OH	43:o:94:PRO:CG	2.37	0.72
27:A:1611:A:H2	35:g:17:ARG:HH21	0.74	0.72
26:4:58:VAL:CG2	48:t:64:GLU:HG2	2.20	0.72
27:A:329:U:O2	27:A:446:G:O6	2.07	0.72
42:n:39:ILE:HG12	42:n:52:GLN:HG2	1.72	0.72
4:H:119:ARG:NE	42:n:6:GLY:O	2.23	0.72
27:A:2883:G:N2	27:A:2886:A:OP2	2.19	0.72
12:S:105:LYS:NZ	29:a:1448:G:OP2	2.21	0.72
24:7:28:ARG:NH2	27:A:210:G:OP1	2.22	0.72
30:b:79:VAL:HG12	30:b:80:VAL:HG23	1.71	0.72
29:a:1299:C:C5'	43:o:48:LEU:HD21	2.19	0.72
26:4:36:GLU:OE2	42:n:50:ASP:C	2.32	0.71
27:A:337:U:O2	27:A:344:G:N2	2.18	0.71
51:w:245:ARG:HE	51:w:249:HIS:HB2	1.55	0.71
29:a:1360:A:O2'	36:h:2:PRO:HG2	1.91	0.71
29:a:1040:U:OP2	32:d:2:GLY:HA3	1.89	0.71
30:b:22:PHE:CE1	30:b:26:ILE:HD11	2.25	0.71
29:a:964:U:H5''	43:o:6:LYS:HE2	1.72	0.71
30:b:130:VAL:HA	30:b:140:LEU:HA	1.73	0.71
26:4:36:GLU:O	42:n:54:THR:HG22	1.90	0.71
29:a:1298:G:OP2	43:o:29:ARG:NH2	2.23	0.71
30:b:57:TYR:OH	50:c:36:ASN:ND2	2.23	0.71
50:c:8:GLN:HG3	50:c:212:LEU:HD11	1.73	0.71
16:W:18:GLU:N	16:W:18:GLU:OE2	2.22	0.70
32:d:12:LEU:CD2	43:o:91:GLY:CA	2.69	0.70
50:c:6:MET:SD	50:c:7:LYS:NZ	2.64	0.70
8:N:93:PRO:HG3	8:N:114:ILE:HG12	1.72	0.70
34:f:63:ILE:HD12	34:f:73:VAL:HG22	1.74	0.70
51:w:124:PHE:CE2	51:w:126:ARG:CD	2.75	0.70
27:A:1426:G:N2	27:A:1426:G:OP2	2.21	0.70
29:a:598:C:C2	45:q:12:LYS:NZ	2.59	0.70
29:a:654:G:H2'	29:a:655:A:H8	1.56	0.70
32:d:139:SER:OG	32:d:142:ARG:NH2	2.24	0.70
17:X:4:HIS:NE2	27:A:81:A:OP1	2.24	0.70
22:5:16:ARG:NH2	27:A:1379:G:OP1	2.22	0.70
27:A:499:G:OP2	27:A:2630:A:O2'	2.09	0.70
27:A:1863:G:H5''	27:A:1864:U:H5'	1.72	0.70
26:4:58:VAL:HG23	48:t:64:GLU:HG2	1.74	0.69
29:a:693:G:H2'	29:a:694:G:C8	2.26	0.69
9:O:61:LEU:O	25:8:13:ARG:NE	2.25	0.69
3:G:139:LYS:NZ	27:A:401:C:OP2	2.19	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:664:U:O2'	40:l:50:VAL:O	2.11	0.69
4:H:53:ASP:OD2	4:H:55:LYS:NZ	2.24	0.69
26:4:36:GLU:OE2	42:n:53:VAL:CG2	2.41	0.69
26:4:61:PHE:CZ	48:t:41:ILE:HD12	2.27	0.69
39:k:6:ILE:HG13	39:k:76:ILE:HD11	1.75	0.69
23:6:12:THR:HG23	23:6:24:ILE:HG22	1.75	0.69
27:A:2422:A:N1	27:A:2450:C:N4	2.40	0.69
29:a:309:G:OP1	45:q:28:ARG:NH2	2.22	0.69
29:a:1299:C:N3	43:o:53:ARG:NH1	2.40	0.69
18:Z:32:LYS:HB3	27:A:759:G:C6	2.26	0.69
27:A:2674:A:N6	27:A:2725:C:C2	2.61	0.69
29:a:517:G:OP1	41:m:110:ARG:NH2	2.26	0.69
29:a:653:G:H2'	29:a:654:G:C8	2.27	0.69
45:q:103:LEU:O	45:q:107:ASN:ND2	2.26	0.69
38:j:133:ARG:HG3	43:o:101:TRP:HE1	1.57	0.69
29:a:99:U:OP1	49:u:12:ARG:NH1	2.26	0.68
36:h:12:LEU:O	36:h:21:GLN:NE2	2.26	0.68
22:5:37:ARG:HD3	22:5:54:LEU:HD22	1.74	0.68
29:a:12:A:C5	33:e:201:LYS:HG3	2.28	0.68
29:a:297:G:N2	29:a:300:A:OP2	2.24	0.68
27:A:1541:G:H2'	27:A:1542:A:H8	1.59	0.68
9:O:65:LYS:HD3	27:A:2640:G:H5''	1.75	0.68
27:A:2137:A:H1'	51:w:75:ARG:NH2	2.08	0.68
27:A:2106:A:H3'	27:A:2107:G:H5''	1.76	0.68
27:A:1560:U:C2	35:g:17:ARG:HD3	2.28	0.67
29:a:1231:A:H2'	29:a:1232:A:C8	2.30	0.67
27:A:334:G:N2	27:A:347:U:O2	2.20	0.67
10:Q:14:SER:OG	27:A:2913:U:O2'	2.12	0.67
27:A:1562:C:N4	27:A:1608:U:H3	1.82	0.67
12:S:93:ARG:NH1	27:A:1971:C:OP1	2.27	0.67
13:T:73:ASP:O	13:T:114:ARG:NH2	2.27	0.67
48:t:41:ILE:HG22	48:t:43:ASP:H	1.57	0.67
27:A:989:G:O6	27:A:990:G:N2	2.27	0.67
27:A:2394:A:O2'	27:A:2396:A:OP1	2.13	0.67
4:H:122:ARG:HD2	42:n:72:ARG:HH22	1.51	0.67
37:i:50:ARG:HH12	37:i:63:GLN:HE22	1.41	0.67
4:H:84:PHE:HB3	27:A:2535:A:C2	2.29	0.67
29:a:437:U:O2'	33:e:115:HIS:ND1	2.27	0.67
27:A:176:G:OP2	27:A:176:G:N2	2.23	0.67
29:a:83:U:O2	29:a:86:G:C6	2.47	0.67
30:b:100:LEU:HD12	30:b:102:LEU:HD21	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:k:68:ARG:CZ	43:o:97:ARG:NH2	2.54	0.67
27:A:2342:A:N6	27:A:2390:U:O2'	2.28	0.67
29:a:985:G:H2'	29:a:986:G:C8	2.30	0.67
32:d:28:TYR:OH	43:o:94:PRO:HG2	1.95	0.67
27:A:1147:A:N6	27:A:1243:G:O2'	2.28	0.66
27:A:1542:A:H61	27:A:1628:A:H1'	1.60	0.66
43:o:53:ARG:O	43:o:56:SER:OG	2.13	0.66
46:r:21:LYS:HB2	46:r:78:GLU:HG3	1.75	0.66
29:a:1018:C:H2'	29:a:1019:U:C6	2.31	0.66
35:g:28:ASN:OD1	35:g:29:VAL:N	2.29	0.66
48:t:25:LYS:HE2	48:t:27:THR:HB	1.77	0.66
6:J:3:LEU:HD13	6:J:36:ALA:HB1	1.77	0.66
27:A:1560:U:O2'	35:g:17:ARG:HG3	1.95	0.66
29:a:719:C:P	35:g:2:ARG:HH22	2.18	0.66
26:4:34:VAL:HG12	42:n:50:ASP:OD2	1.95	0.66
27:A:1611:A:H2	35:g:17:ARG:CZ	2.02	0.66
29:a:1338:G:H2'	29:a:1339:A:C8	2.31	0.66
38:j:133:ARG:HG3	43:o:101:TRP:CD1	2.31	0.66
29:a:254:G:OP1	46:r:85:THR:OG1	2.13	0.66
29:a:593:C:OP1	33:e:76:ARG:NH1	2.25	0.66
49:u:45:ASP:OD1	49:u:45:ASP:N	2.28	0.66
4:H:15:TYR:HA	4:H:19:ILE:HB	1.76	0.66
27:A:159:A:N3	27:A:2431:C:O2'	2.27	0.66
27:A:1609:G:H2'	27:A:1610:C:H6	1.60	0.66
30:b:115:THR:O	30:b:119:LEU:HG	1.94	0.66
20:2:28:GLU:OE1	20:2:46:ARG:NH2	2.27	0.66
27:A:539:C:N4	27:A:542:A:OP2	2.26	0.66
27:A:2482:U:O2'	27:A:2651:C:OP2	2.13	0.66
29:a:485:G:H2'	29:a:486:G:C8	2.31	0.66
29:a:1199:C:H2'	29:a:1200:A:H8	1.58	0.66
29:a:1199:C:H2'	29:a:1200:A:C8	2.31	0.66
40:l:121:ASP:HB2	51:w:223:LEU:CD1	2.26	0.66
29:a:789:G:OP2	44:p:48:HIS:NE2	2.29	0.66
29:a:1017:C:H2'	29:a:1018:C:C6	2.30	0.66
29:a:1057:G:N2	29:a:1060:A:OP2	2.25	0.66
27:A:1165:G:H4'	27:A:1166:A:H5'	1.79	0.65
29:a:25:G:H2'	29:a:26:G:C8	2.31	0.65
17:X:94:LYS:NZ	27:A:377:C:O3'	2.26	0.65
27:A:2674:A:OP1	27:A:2721:A:O2'	2.12	0.65
27:A:567:A:H4'	27:A:568:A:H5'	1.78	0.65
32:d:23:TYR:HB2	39:k:94:ALA:O	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2552:A:H2'	27:A:2553:G:C8	2.32	0.65
29:a:1051:C:H2'	29:a:1052:G:H8	1.62	0.65
17:X:37:GLY:HA2	17:X:40:ARG:HH21	1.62	0.65
29:a:12:A:N7	33:e:201:LYS:HA	2.12	0.65
29:a:1014:U:H2'	29:a:1015:G:C8	2.31	0.65
29:a:1299:C:C4'	43:o:48:LEU:HD21	2.26	0.65
30:b:129:THR:O	30:b:141:ASP:N	2.30	0.65
33:e:49:GLN:HB3	33:e:198:LEU:HB2	1.78	0.65
36:h:116:MET:HE2	36:h:116:MET:HA	1.77	0.65
29:a:127:A:OP2	46:r:80:ARG:HG2	1.96	0.65
29:a:1027:G:HO2'	29:a:1196:G:HO2'	1.43	0.65
39:k:42:LEU:HB2	39:k:71:LYS:HB2	1.79	0.65
43:o:49:GLN:CD	48:t:10:PHE:CE1	2.75	0.65
9:O:74:GLU:OE1	9:O:74:GLU:N	2.29	0.65
15:V:69:GLU:N	15:V:69:GLU:OE2	2.31	0.65
29:a:489:A:H8	29:a:523:U:HO2'	1.45	0.65
29:a:1015:G:H2'	29:a:1016:G:H8	1.59	0.65
27:A:365:U:H3	27:A:437:G:H1	1.45	0.64
28:B:67:A:H4'	28:B:68:G:H5'	1.79	0.64
29:a:956:A:C5	43:o:71:ARG:NH1	2.65	0.64
29:a:1010:C:N4	29:a:1014:U:H3	1.94	0.64
3:G:179:SER:OG	3:G:181:ASP:OD1	2.14	0.64
17:X:63:GLU:N	17:X:63:GLU:OE2	2.30	0.64
23:6:25:THR:HG21	27:A:2510:A:H62	1.61	0.64
51:w:131:ARG:HD2	51:w:250:TYR:CZ	2.31	0.64
27:A:2332:U:N3	27:A:2333:G:O6	2.30	0.64
27:A:3034:C:H2'	27:A:3035:C:H6	1.62	0.64
29:a:203:U:H2'	29:a:204:A:H8	1.62	0.64
2:F:60:ARG:NH2	27:A:3052:A:OP1	2.22	0.64
2:F:174:ARG:NE	27:A:2997:C:OP1	2.29	0.64
24:7:38:ARG:CZ	27:A:50:A:C2	2.80	0.64
29:a:195:U:O2	46:r:80:ARG:NH2	2.31	0.64
29:a:207:G:O2'	49:u:59:ASP:OD2	2.14	0.64
5:I:150:ARG:HD2	5:I:163:VAL:HG23	1.79	0.64
43:o:49:GLN:CD	48:t:10:PHE:HE1	2.06	0.64
1:E:108:PRO:HD2	1:E:111:LEU:HD22	1.79	0.64
10:Q:70:ILE:HG22	10:Q:72:ASP:H	1.62	0.64
37:i:40:LEU:HD21	37:i:131:VAL:HG11	1.80	0.64
29:a:694:G:H2'	29:a:695:A:C8	2.32	0.64
27:A:1500:A:O2'	27:A:1511:U:O2	2.15	0.64
30:b:117:GLU:HA	30:b:120:LYS:HG2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:o:23:ARG:HD2	43:o:24:ARG:HG2	1.78	0.64
50:c:32:PHE:HB2	50:c:42:ASP:HB2	1.79	0.64
51:w:131:ARG:O	51:w:249:HIS:ND1	2.29	0.64
11:R:14:ARG:HH11	28:B:48:C:P	2.21	0.64
26:4:60:ARG:NH2	29:a:1293:G:H5'	2.07	0.64
32:d:99:GLN:NE2	32:d:101:ASN:OD1	2.31	0.64
27:A:1476:G:H2'	27:A:1477:C:C6	2.33	0.63
27:A:1710:A:H61	27:A:1716:A:H5''	1.63	0.63
29:a:956:A:H5'	43:o:71:ARG:HD3	1.80	0.63
27:A:1886:A:N3	27:A:1888:C:N4	2.46	0.63
45:q:86:LEU:HB2	45:q:87:PRO:HD3	1.80	0.63
4:H:80:SER:HB2	4:H:87:ARG:HE	1.64	0.63
27:A:2351:A:N3	27:A:2396:A:O2'	2.31	0.63
29:a:1342:A:C8	43:o:58:VAL:HG23	2.33	0.63
51:w:161:HIS:HE1	51:w:163:PHE:HB3	1.62	0.63
9:O:89:GLN:OE1	9:O:89:GLN:N	2.25	0.63
23:6:39:LYS:HA	23:6:50:PRO:HA	1.80	0.63
38:j:72:LEU:HD23	38:j:107:LEU:HD11	1.81	0.63
21:3:58:GLU:OE1	21:3:58:GLU:N	2.30	0.63
27:A:271:A:OP2	27:A:314:G:N2	2.29	0.63
27:A:1547:G:N2	27:A:1623:U:O2	2.28	0.63
29:a:452:A:C2	45:q:47:SER:HB3	2.33	0.63
6:J:9:VAL:HG13	6:J:12:LEU:HB2	1.78	0.63
18:Z:64:PRO:HB3	27:A:759:G:H1	1.62	0.63
21:3:57:GLU:OE1	21:3:57:GLU:N	2.32	0.63
27:A:990:G:O6	27:A:1018:U:O4	2.17	0.63
27:A:1610:C:H2'	27:A:1611:A:H8	1.60	0.63
27:A:2756:G:O2'	27:A:2881:A:N1	2.30	0.63
29:a:411:A:C4	29:a:413:G:H1'	2.34	0.63
29:a:438:U:O2'	29:a:439:U:O2	2.14	0.63
29:a:873:U:H2'	29:a:874:A:H8	1.64	0.63
29:a:1410:C:H2'	29:a:1411:A:H8	1.63	0.63
38:j:26:ILE:HD11	38:j:41:LEU:HB3	1.81	0.63
39:k:66:GLU:OE1	39:k:66:GLU:N	2.32	0.63
45:q:90:GLU:N	45:q:90:GLU:OE2	2.31	0.63
24:7:11:ASN:ND2	27:A:885:G:OP1	2.32	0.63
26:4:37:VAL:HB	42:n:57:ARG:NH2	2.07	0.63
43:o:32:ARG:HA	43:o:39:GLU:HG2	1.80	0.63
26:4:58:VAL:HG22	48:t:67:VAL:HG21	1.81	0.63
45:q:46:PRO:HG3	45:q:96:LYS:HD3	1.80	0.63
51:w:153:MET:HE3	51:w:161:HIS:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1207:C:OP2	42:n:103:THR:OG1	2.17	0.62
29:a:1351:G:OP2	38:j:134:LYS:HD3	1.99	0.62
29:a:1506:U:H2'	29:a:1507:G:H8	1.63	0.62
39:k:63:GLU:CD	43:o:85:ARG:HH11	2.07	0.62
26:4:36:GLU:CG	42:n:53:VAL:CB	2.59	0.62
42:n:33:ILE:O	42:n:37:THR:HG22	1.99	0.62
4:H:122:ARG:CD	42:n:72:ARG:NH2	2.47	0.62
27:A:273:A:H62	27:A:313:G:H21	1.46	0.62
27:A:384:G:H2'	27:A:385:G:H8	1.64	0.62
32:d:130:ARG:NH1	34:f:80:GLU:OE2	2.32	0.62
21:3:15:ALA:O	21:3:20:ARG:NH1	2.32	0.62
27:A:2372:U:H2'	27:A:2373:G:C8	2.34	0.62
29:a:312:C:H2'	29:a:313:A:H8	1.64	0.62
29:a:1291:G:H8	42:n:99:ARG:NH2	1.96	0.62
29:a:401:C:O2'	29:a:601:A:N3	2.30	0.62
27:A:218:A:N3	27:A:234:U:O2'	2.32	0.62
27:A:2371:G:H2'	27:A:2372:U:C6	2.35	0.62
29:a:209:A:N3	29:a:222:U:O2'	2.29	0.62
30:b:143:GLY:O	30:b:144:LEU:HD23	2.00	0.62
39:k:21:SER:HA	39:k:24:LYS:NZ	2.15	0.62
27:A:1561:C:C4'	35:g:17:ARG:HH12	2.12	0.62
27:A:2682:G:H21	27:A:2683:A:H61	1.47	0.62
27:A:2819:G:N2	27:A:2822:A:OP2	2.25	0.62
29:a:144:G:H2'	29:a:145:G:C8	2.35	0.62
29:a:1407:U:H2'	29:a:1408:A:C8	2.35	0.62
26:4:37:VAL:H	42:n:57:ARG:NH2	1.92	0.62
27:A:2248:C:H2'	27:A:2249:G:H8	1.64	0.62
29:a:1522:C:H2'	29:a:1523:C:O4'	2.00	0.62
46:r:73:ARG:HB2	46:r:95:GLU:HG3	1.81	0.62
50:c:186:ILE:HG22	50:c:200:ILE:HB	1.82	0.62
2:F:19:GLU:N	2:F:19:GLU:OE1	2.32	0.62
11:R:14:ARG:NH1	28:B:48:C:OP2	2.32	0.62
27:A:1755:A:O2'	27:A:1758:G:N2	2.28	0.62
27:A:2224:C:O2'	27:A:2913:U:OP2	2.17	0.62
27:A:2470:A:H2'	27:A:2471:A:H8	1.63	0.62
29:a:872:G:O2'	29:a:888:A:N6	2.32	0.62
42:n:51:ASP:OD1	42:n:52:GLN:N	2.33	0.62
16:W:68:ARG:NH2	27:A:1449:C:OP1	2.31	0.61
27:A:551:G:N2	27:A:554:A:OP2	2.29	0.61
27:A:2674:A:N6	27:A:2725:C:O2	2.33	0.61
27:A:2752:U:O2'	27:A:2754:G:OP1	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:362:G:N2	29:a:365:U:OP2	2.33	0.61
18:Z:18:ALA:HB1	27:A:2495:G:OP1	1.99	0.61
27:A:1556:A:N1	27:A:1615:G:O6	2.33	0.61
27:A:1562:C:H2'	27:A:1563:A:H4'	1.81	0.61
29:a:1290:C:OP2	42:n:101:GLN:NE2	2.30	0.61
1:E:224:VAL:HG13	27:A:2043:C:OP1	2.00	0.61
5:I:58:ASP:O	5:I:63:ARG:NH1	2.33	0.61
27:A:2176:A:N3	27:A:2784:C:O2'	2.33	0.61
32:d:39:ARG:NH1	32:d:54:VAL:O	2.34	0.61
5:I:108:LEU:HD21	5:I:153:ARG:HD2	1.83	0.61
27:A:389:G:N1	27:A:392:A:OP2	2.27	0.61
27:A:1754:G:N1	27:A:1759:A:N6	2.47	0.61
34:f:108:HIS:CD2	37:i:101:LEU:HD12	2.35	0.61
4:H:61:ILE:HD12	4:H:72:PRO:HG2	1.81	0.61
20:2:13:LEU:HB3	20:2:17:GLU:HG3	1.83	0.61
29:a:38:C:H2'	29:a:39:G:H8	1.66	0.61
50:c:6:MET:SD	50:c:6:MET:N	2.72	0.61
19:1:14:PHE:CG	27:A:187:G:H5''	2.35	0.61
26:4:65:TYR:CG	48:t:9:PRO:HD3	2.35	0.61
27:A:308:U:H2'	27:A:309:G:H8	1.65	0.61
27:A:2137:A:C2	29:a:1477:A:N7	2.69	0.61
29:a:692:A:H2'	29:a:693:G:C8	2.35	0.61
5:I:87:LYS:HD2	5:I:88:MET:N	2.15	0.61
27:A:2344:G:H4'	27:A:2391:G:H22	1.66	0.61
27:A:3078:G:N2	27:A:3081:A:OP2	2.29	0.61
48:t:19:VAL:HG21	48:t:44:PHE:HE1	1.64	0.61
1:E:244:ARG:NH2	27:A:2463:G:OP1	2.30	0.61
11:R:14:ARG:HD3	28:B:48:C:OP1	1.99	0.61
15:V:90:LYS:HB3	15:V:102:ARG:HD2	1.82	0.61
27:A:813:C:O2'	27:A:849:A:N6	2.31	0.61
27:A:1921:G:H2'	27:A:1922:G:H8	1.66	0.61
27:A:2064:A:H8	27:A:2065:A:H62	1.47	0.61
27:A:3014:A:N6	27:A:3113:A:OP2	2.34	0.61
29:a:485:G:H2'	29:a:486:G:H8	1.64	0.61
29:a:983:C:H2'	29:a:984:A:C8	2.35	0.61
29:a:1219:A:H5'	29:a:1318:C:H41	1.66	0.61
24:7:37:ARG:NH1	24:7:44:ALA:O	2.34	0.61
27:A:1637:G:HO2'	27:A:1805:G:HO2'	1.47	0.61
27:A:2805:G:N2	27:A:2805:G:OP2	2.33	0.61
29:a:669:C:OP1	40:l:55:SER:OG	2.18	0.61
42:n:58:ASP:OD1	42:n:59:TYR:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:7:10:PRO:HG2	27:A:1424:G:H4'	1.82	0.61
27:A:1560:U:O2'	35:g:17:ARG:CG	2.49	0.61
29:a:1231:A:N3	29:a:1353:G:O2'	2.31	0.61
47:s:46:GLY:O	47:s:72:ARG:NH2	2.34	0.61
29:a:1410:C:H2'	29:a:1411:A:C8	2.36	0.60
47:s:57:CYS:SG	47:s:60:HIS:ND1	2.74	0.60
29:a:880:G:N2	29:a:883:A:OP2	2.34	0.60
27:A:929:C:H1'	27:A:1339:G:H21	1.66	0.60
27:A:2902:A:H2'	27:A:2903:A:C8	2.37	0.60
29:a:1106:U:OP1	39:k:7:ARG:NH2	2.35	0.60
39:k:15:HIS:ND1	39:k:16:GLU:OE2	2.34	0.60
27:A:2407:C:N4	27:A:2408:G:O6	2.34	0.60
29:a:928:A:H2'	29:a:929:G:C8	2.36	0.60
29:a:1298:G:OP1	43:o:29:ARG:NH1	2.34	0.60
27:A:239:U:HO2'	27:A:716:G:HO2'	1.37	0.60
29:a:21:U:H2'	29:a:22:C:C6	2.36	0.60
5:I:104:LEU:HD21	5:I:132:PHE:HE2	1.66	0.60
6:J:12:LEU:HD22	6:J:19:VAL:HG11	1.82	0.60
26:4:15:GLN:N	26:4:33:ILE:O	2.33	0.60
27:A:1530:G:H21	27:A:1805:G:H22	1.49	0.60
51:w:49:GLU:HG2	51:w:50:ARG:HG3	1.84	0.60
27:A:2211:C:H2'	27:A:2212:A:H8	1.67	0.60
32:d:20:SER:OG	32:d:22:TRP:NE1	2.35	0.60
46:r:72:ASP:OD2	46:r:96:LYS:NZ	2.33	0.60
41:m:4:ILE:HG22	46:r:51:LYS:HD2	1.83	0.60
12:S:1:MET:HE1	12:S:3:THR:HA	1.84	0.60
29:a:716:U:O2'	35:g:90:VAL:O	2.20	0.60
45:q:54:GLU:OE2	45:q:54:GLU:N	2.24	0.60
21:3:37:ARG:HH22	27:A:1043:G:H4'	1.66	0.60
27:A:1018:U:O2	27:A:1019:C:N4	2.34	0.60
27:A:1543:A:N1	27:A:1628:A:O2'	2.34	0.60
43:o:21:ALA:HA	43:o:25:ALA:HB3	1.84	0.60
19:1:32:ASN:HB2	27:A:485:U:H5''	1.84	0.59
37:i:48:ASP:OD1	37:i:49:TYR:N	2.35	0.59
38:j:54:THR:HG23	38:j:56:GLU:H	1.67	0.59
39:k:63:GLU:OE2	43:o:85:ARG:NH1	2.34	0.59
51:w:126:ARG:HB2	51:w:248:GLY:HA3	1.83	0.59
27:A:681:C:H2'	27:A:682:A:H8	1.67	0.59
27:A:2144:C:OP1	29:a:1501:G:C8	2.55	0.59
29:a:192:G:O2'	46:r:17:ARG:NH1	2.35	0.59
7:M:141:GLU:O	7:M:143:LYS:NZ	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:N:17:LYS:HE3	8:N:47:ILE:HG13	1.83	0.59
13:T:37:GLU:OE2	27:A:1367:G:N1	2.27	0.59
14:U:26:LYS:HA	14:U:95:THR:HG23	1.83	0.59
27:A:220:A:H2	27:A:266:U:H5''	1.67	0.59
27:A:830:A:OP1	44:p:64:ARG:NH1	2.36	0.59
27:A:2074:G:H21	27:A:2109:A:H62	1.49	0.59
48:t:29:GLN:OE1	48:t:29:GLN:N	2.35	0.59
4:H:143:SER:OG	42:n:3:ARG:NH1	2.35	0.59
27:A:1640:A:H2'	27:A:1642:G:N7	2.18	0.59
27:A:2879:G:O2'	27:A:2888:G:O6	2.17	0.59
32:d:130:ARG:NH2	34:f:80:GLU:CD	2.61	0.59
16:W:62:ARG:NH2	27:A:1455:U:OP2	2.35	0.59
27:A:1554:U:H2'	27:A:1555:A:C8	2.38	0.59
27:A:857:U:H2'	27:A:858:A:C8	2.37	0.59
27:A:1530:G:N2	27:A:1805:G:H1	2.01	0.59
27:A:2425:U:O2'	27:A:2427:G:OP1	2.21	0.59
30:b:28:LYS:HZ1	50:c:35:ARG:HH22	1.48	0.59
30:b:140:LEU:HD21	30:b:169:ILE:HG22	1.85	0.59
36:h:81:GLY:HA2	51:w:114:GLU:O	2.02	0.59
32:d:27:GLN:OE1	32:d:27:GLN:N	2.35	0.59
37:i:10:PHE:HD2	37:i:36:ILE:HD11	1.68	0.59
4:H:144:MET:SD	4:H:144:MET:N	2.75	0.59
14:U:12:LYS:NZ	27:A:1112:C:O2	2.35	0.59
27:A:1165:G:O2'	27:A:1228:A:N6	2.26	0.59
1:E:132:PRO:HA	1:E:190:ARG:HA	1.85	0.59
27:A:114:G:OP2	27:A:116:A:O2'	2.20	0.59
27:A:974:G:H4'	27:A:975:U:O5'	2.03	0.59
27:A:1696:G:O2'	27:A:1736:G:O6	2.20	0.59
27:A:2677:A:O2'	27:A:2796:A:N3	2.35	0.59
5:I:87:LYS:HD2	5:I:88:MET:H	1.68	0.59
8:N:2:ILE:HG21	8:N:8:LEU:HD11	1.84	0.59
21:3:5:LYS:HE2	21:3:34:SER:HB3	1.84	0.59
26:4:36:GLU:OE2	42:n:53:VAL:HG23	2.02	0.59
11:R:90:GLU:HA	11:R:93:LYS:HB2	1.84	0.58
27:A:255:A:O2'	27:A:472:C:OP2	2.21	0.58
29:a:1149:C:O2'	29:a:1150:A:OP2	2.20	0.58
41:m:74:LEU:HD21	41:m:104:THR:HB	1.85	0.58
50:c:47:LEU:HA	50:c:50:ILE:HG22	1.83	0.58
50:c:72:THR:N	50:c:169:GLU:OE2	2.31	0.58
27:A:911:U:H2'	27:A:912:C:C6	2.38	0.58
27:A:1035:G:H21	27:A:2493:A:H8	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:269:U:H2'	29:a:270:A:C8	2.38	0.58
29:a:452:A:H2	45:q:47:SER:HB3	1.67	0.58
29:a:826:U:H2'	29:a:828:G:H5'	1.85	0.58
35:g:12:PRO:O	35:g:45:ARG:NH2	2.35	0.58
35:g:83:GLU:OE2	35:g:83:GLU:N	2.26	0.58
48:t:32:LYS:HA	48:t:50:ALA:HB3	1.85	0.58
29:a:1324:C:H2'	29:a:1325:G:H8	1.68	0.58
26:4:14:VAL:HB	26:4:22:PHE:HB3	1.86	0.58
27:A:990:G:H1	27:A:1018:U:H3	0.79	0.58
27:A:2902:A:H2'	27:A:2903:A:H8	1.67	0.58
29:a:810:G:H4'	50:c:21:ARG:O	2.04	0.58
27:A:1468:A:H2'	27:A:1469:A:H8	1.69	0.58
29:a:748:A:H4'	29:a:1507:G:N2	2.18	0.58
29:a:1342:A:C5	43:o:58:VAL:CG2	2.86	0.58
29:a:1517:C:H5'	29:a:1518:A:H5'	1.86	0.58
35:g:44:GLY:HA2	35:g:60:TYR:H	1.68	0.58
48:t:13:ASP:O	48:t:17:LYS:HG3	2.03	0.58
20:2:9:GLU:HA	20:2:12:GLU:HG2	1.85	0.58
27:A:285:U:H3'	27:A:286:G:H4'	1.86	0.58
27:A:2043:C:O2'	27:A:2195:U:OP2	2.21	0.58
34:f:130:VAL:O	34:f:137:ARG:NH2	2.36	0.58
37:i:26:THR:HG23	37:i:61:VAL:HG22	1.85	0.58
51:w:56:ALA:HB2	51:w:81:LEU:HD21	1.86	0.58
9:O:97:GLU:N	9:O:97:GLU:OE2	2.35	0.58
27:A:337:U:O4	27:A:344:G:O6	2.22	0.58
27:A:473:C:O2'	27:A:476:G:N2	2.37	0.58
43:o:22:GLU:HB3	43:o:23:ARG:CZ	2.33	0.58
49:u:46:LYS:HA	49:u:49:GLU:OE1	2.02	0.58
1:E:143:HIS:ND1	1:E:194:GLY:O	2.29	0.58
10:Q:10:LEU:HB2	10:Q:17:GLN:HG3	1.85	0.58
15:V:53:PRO:O	15:V:57:VAL:HG23	2.04	0.58
24:7:14:ARG:NH2	27:A:885:G:OP2	2.37	0.58
27:A:1562:C:H2'	27:A:1563:A:C4'	2.34	0.58
29:a:21:U:H2'	29:a:22:C:H6	1.69	0.58
34:f:83:ALA:O	34:f:87:LYS:HG3	2.03	0.58
29:a:654:G:H2'	29:a:655:A:C8	2.38	0.58
29:a:953:G:N2	29:a:1346:A:OP1	2.28	0.58
29:a:1232:A:N3	29:a:1352:C:O2'	2.36	0.58
48:t:39:THR:HG22	48:t:70:LYS:HE2	1.84	0.58
29:a:92:A:O2'	29:a:93:C:O5'	2.22	0.58
29:a:1130:C:H2'	29:a:1131:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1132:U:O2	39:k:41:PRO:HG3	2.04	0.58
42:n:39:ILE:HD12	42:n:39:ILE:H	1.69	0.58
1:E:88:ARG:NH2	27:A:2034:G:OP1	2.35	0.57
27:A:2552:A:H2'	27:A:2553:G:H8	1.66	0.57
29:a:688:C:H2'	29:a:689:A:H8	1.68	0.57
27:A:191:G:N2	27:A:191:G:OP2	2.36	0.57
27:A:1540:U:O4	27:A:1632:G:O6	2.23	0.57
27:A:2870:C:OP2	27:A:2956:G:O2'	2.21	0.57
1:E:60:ARG:HA	27:A:1788:G:H5'	1.86	0.57
24:7:38:ARG:CZ	27:A:50:A:H2	2.17	0.57
27:A:284:G:H1'	27:A:303:G:C2	2.39	0.57
27:A:357:U:H4'	27:A:358:G:O5'	2.05	0.57
27:A:692:C:H2'	27:A:693:G:H8	1.70	0.57
29:a:380:G:N2	29:a:383:A:OP2	2.33	0.57
10:Q:118:GLU:OE1	10:Q:118:GLU:N	2.38	0.57
12:S:73:PHE:HB3	12:S:80:ILE:HD11	1.85	0.57
27:A:1651:C:H2'	27:A:1652:A:H8	1.69	0.57
27:A:2420:U:H1'	27:A:2421:A:C8	2.39	0.57
27:A:1229:A:H8	27:A:1230:G:H1'	1.69	0.57
27:A:1532:G:O2'	27:A:1803:A:N1	2.34	0.57
27:A:1673:A:H5''	27:A:1674:G:H5''	1.86	0.57
27:A:1677:G:H2'	27:A:1678:U:O4'	2.05	0.57
27:A:2922:U:H2'	27:A:2923:C:C6	2.40	0.57
29:a:312:C:H2'	29:a:313:A:C8	2.39	0.57
32:d:130:ARG:CZ	34:f:80:GLU:CD	2.77	0.57
33:e:94:ASP:OD1	33:e:95:ASN:N	2.38	0.57
22:5:33:ALA:HB3	22:5:35:GLN:HE22	1.68	0.57
27:A:2287:C:H42	27:A:2725:C:H1'	1.68	0.57
29:a:82:U:O2	29:a:87:G:N2	2.28	0.57
29:a:642:C:H2'	29:a:643:A:C8	2.39	0.57
29:a:1476:A:HO2'	51:w:80:ARG:NH2	2.01	0.57
9:O:15:GLU:OE1	9:O:16:LYS:HG2	2.04	0.57
27:A:412:A:HO2'	27:A:413:G:H21	1.51	0.57
27:A:3022:G:H2'	27:A:3023:G:O4'	2.05	0.57
29:a:49:U:H2'	29:a:50:G:C8	2.39	0.57
33:e:104:ARG:H	33:e:108:MET:HE2	1.69	0.57
51:w:185:VAL:HG22	51:w:205:SER:HB2	1.87	0.57
2:F:5:GLY:HA3	2:F:84:LEU:HD21	1.87	0.57
11:R:68:ALA:HA	11:R:71:ARG:HB2	1.85	0.57
26:4:34:VAL:HG12	42:n:50:ASP:CB	2.35	0.57
26:4:65:TYR:CD1	48:t:9:PRO:HD3	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:752:C:H2'	27:A:753:A:H8	1.70	0.57
29:a:1442:G:OP1	49:u:30:THR:OG1	2.20	0.57
40:l:103:GLU:OE2	51:w:224:LEU:C	2.47	0.57
12:S:61:ARG:NH1	12:S:70:GLU:OE1	2.37	0.57
26:4:57:ARG:CD	48:t:67:VAL:O	2.53	0.57
26:4:61:PHE:CE2	48:t:41:ILE:HD12	2.39	0.57
27:A:3057:U:H2'	27:A:3058:A:H8	1.70	0.57
30:b:127:LYS:HD3	30:b:128:GLY:N	2.20	0.57
39:k:80:THR:HG23	39:k:83:THR:H	1.68	0.57
5:I:96:ARG:HH22	5:I:98:GLN:HG2	1.70	0.57
27:A:28:C:O2'	27:A:1353:G:OP1	2.21	0.57
27:A:2047:C:H2'	27:A:2048:G:H8	1.70	0.57
29:a:461:G:O2'	29:a:463:C:N4	2.37	0.57
29:a:1110:A:H4'	38:j:40:ARG:HH11	1.70	0.57
32:d:109:GLU:OE1	32:d:139:SER:OG	2.19	0.56
45:q:81:GLN:O	45:q:85:GLY:N	2.37	0.56
19:l:47:GLN:N	19:l:47:GLN:OE1	2.38	0.56
27:A:1791:A:H2'	27:A:1792:A:H8	1.71	0.56
27:A:2682:G:H21	27:A:2683:A:N6	2.03	0.56
29:a:1120:G:H4'	29:a:1121:G:H5'	1.87	0.56
29:a:1299:C:OP1	43:o:56:SER:HB3	2.05	0.56
29:a:1324:C:H2'	29:a:1325:G:C8	2.39	0.56
32:d:58:ARG:HG3	32:d:63:VAL:HG22	1.87	0.56
33:e:73:GLU:OE1	33:e:76:ARG:NH2	2.35	0.56
12:S:105:LYS:NZ	29:a:1448:G:OP1	2.38	0.56
27:A:808:A:O2'	27:A:1468:A:N3	2.36	0.56
27:A:1705:C:H2'	27:A:1706:A:H8	1.69	0.56
27:A:2470:A:H2'	27:A:2471:A:C8	2.40	0.56
27:A:2758:A:H2'	27:A:2759:G:O4'	2.05	0.56
29:a:92:A:H1'	29:a:93:C:H5	1.69	0.56
29:a:272:C:H2'	29:a:273:A:H8	1.68	0.56
29:a:920:A:N3	29:a:1359:U:O2'	2.31	0.56
29:a:1491:A:H2'	29:a:1492:G:C8	2.41	0.56
32:d:69:THR:HG22	32:d:102:ILE:HD11	1.87	0.56
13:T:12:LYS:O	13:T:16:THR:HG23	2.05	0.56
27:A:1552:A:N6	27:A:1616:A:OP2	2.39	0.56
29:a:890:A:H2'	29:a:891:A:H8	1.71	0.56
29:a:1418:G:H2'	29:a:1419:C:C6	2.41	0.56
27:A:1009:U:H2'	27:A:1010:U:C6	2.41	0.56
27:A:1710:A:N6	27:A:1716:A:OP2	2.39	0.56
27:A:1754:G:H1	27:A:1759:A:N6	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1299:C:H4'	43:o:48:LEU:HD23	1.88	0.56
29:a:1508:C:H2'	29:a:1509:G:H8	1.69	0.56
48:t:15:LEU:HA	48:t:18:LYS:HB2	1.86	0.56
50:c:58:LYS:HG2	50:c:223:GLU:OE1	2.06	0.56
27:A:279:U:H2'	27:A:280:G:H8	1.69	0.56
27:A:2716:U:H2'	27:A:2717:U:C6	2.41	0.56
29:a:691:G:OP1	35:g:54:LYS:NZ	2.26	0.56
29:a:695:A:H2'	29:a:696:A:C8	2.41	0.56
51:w:124:PHE:CE2	51:w:126:ARG:HD3	2.40	0.56
11:R:73:ILE:HG12	11:R:75:GLY:H	1.70	0.56
23:6:15:CYS:SG	23:6:16:GLU:N	2.78	0.56
26:4:34:VAL:C	42:n:50:ASP:OD2	2.49	0.56
33:e:87:ARG:O	33:e:91:SER:OG	2.24	0.56
51:w:124:PHE:CE2	51:w:126:ARG:CG	2.89	0.56
27:A:1468:A:H2'	27:A:1469:A:C8	2.40	0.56
27:A:3071:A:N7	27:A:3089:A:O2'	2.36	0.56
29:a:804:U:H2'	29:a:805:A:H8	1.69	0.56
29:a:884:G:H2'	29:a:885:G:H8	1.70	0.56
50:c:45:GLN:HA	50:c:48:THR:HG22	1.87	0.56
4:H:44:ASN:ND2	27:A:2537:C:O4'	2.39	0.56
5:I:102:GLN:CD	5:I:102:GLN:H	2.14	0.56
30:b:173:ILE:HD12	30:b:183:VAL:HG22	1.88	0.56
35:g:27:LEU:O	35:g:30:ILE:HG13	2.06	0.56
51:w:123:TYR:HD1	51:w:124:PHE:O	1.88	0.56
51:w:124:PHE:HE2	51:w:126:ARG:HD2	1.69	0.56
27:A:639:C:HO2'	27:A:640:G:H8	1.53	0.56
32:d:12:LEU:HD22	43:o:91:GLY:CA	2.28	0.56
50:c:83:GLU:HG3	50:c:214:THR:HB	1.88	0.56
7:M:27:ARG:HH22	27:A:1260:C:HO2'	1.52	0.55
27:A:935:A:H4'	27:A:951:G:N2	2.20	0.55
27:A:1825:C:N4	27:A:1840:G:OP2	2.31	0.55
27:A:2682:G:O2'	27:A:2684:U:O4	2.24	0.55
40:l:47:GLN:OE1	40:l:47:GLN:N	2.38	0.55
40:l:99:GLY:HA2	40:l:102:ARG:HD3	1.87	0.55
43:o:43:ALA:HB1	43:o:46:SER:HB2	1.88	0.55
4:H:110:LEU:HD12	4:H:114:ALA:HB3	1.87	0.55
27:A:34:C:H2'	27:A:35:A:C8	2.41	0.55
27:A:353:G:O6	27:A:442:U:O2	2.25	0.55
27:A:429:A:H2'	27:A:430:A:H8	1.70	0.55
27:A:664:A:H3'	27:A:665:G:H8	1.72	0.55
30:b:66:ARG:NH2	30:b:72:HIS:HA	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:b:69:SER:HB3	30:b:74:VAL:HG21	1.89	0.55
32:d:137:ILE:O	32:d:141:MET:HG2	2.05	0.55
40:l:52:ALA:HB1	40:l:82:LYS:HB3	1.87	0.55
50:c:121:GLU:OE1	50:c:122:GLN:NE2	2.40	0.55
6:j:10:GLU:OE2	6:j:11:HIS:N	2.40	0.55
27:A:380:A:N1	27:A:404:A:O2'	2.35	0.55
27:A:2764:C:O2'	27:A:2964:A:N3	2.33	0.55
29:a:1159:G:N2	29:a:1162:G:OP2	2.38	0.55
46:r:67:GLU:OE1	46:r:67:GLU:N	2.38	0.55
15:V:23:LYS:NZ	27:A:2236:G:N7	2.55	0.55
27:A:2271:C:H2'	27:A:2272:G:H8	1.72	0.55
27:A:2356:G:H2'	27:A:2380:G:H1	1.71	0.55
29:a:1138:A:H62	29:a:1159:G:H21	1.55	0.55
36:h:138:ARG:NH1	36:h:139:GLU:OE2	2.39	0.55
11:R:37:ARG:NH2	11:R:54:ASP:OD1	2.38	0.55
29:a:819:U:H3	29:a:829:G:H1	1.54	0.55
33:e:176:LEU:HB3	45:q:106:PHE:HE1	1.71	0.55
27:A:1560:U:H3'	27:A:1561:C:C6	2.42	0.55
27:A:2238:A:H2'	27:A:2239:A:C8	2.42	0.55
27:A:2367:G:N2	27:A:2369:C:O2	2.40	0.55
21:3:8:GLN:HB2	21:3:28:LEU:HD13	1.88	0.55
27:A:380:A:N3	27:A:401:C:O2'	2.36	0.55
27:A:470:G:N2	27:A:481:C:N3	2.55	0.55
27:A:1396:G:H2'	27:A:1397:U:C6	2.42	0.55
27:A:1476:G:H2'	27:A:1477:C:H6	1.70	0.55
29:a:806:C:O2	37:i:16:ASN:ND2	2.40	0.55
51:w:182:TYR:HB2	51:w:202:ILE:HG22	1.88	0.55
13:T:53:ARG:HH11	27:A:1113:C:P	2.30	0.55
26:4:16:CYS:SG	26:4:17:GLY:N	2.79	0.55
32:d:87:ARG:O	32:d:91:GLU:HG2	2.06	0.55
33:e:145:LEU:O	33:e:154:ARG:NH2	2.40	0.55
35:g:21:PRO:O	35:g:24:GLU:HB3	2.06	0.55
50:c:79:SER:O	50:c:82:GLU:HG3	2.07	0.55
50:c:156:LYS:HD2	50:c:157:VAL:HG12	1.88	0.55
22:5:14:ARG:HB3	27:A:13:G:H5''	1.87	0.55
28:B:10:G:O2'	28:B:11:U:OP1	2.20	0.55
29:a:632:U:O4	29:a:732:G:O2'	2.22	0.55
29:a:1010:C:H42	29:a:1014:U:H3	1.49	0.55
29:a:1132:U:O4'	39:k:41:PRO:HB2	2.07	0.55
5:I:153:ARG:HE	5:I:154:ARG:H	1.55	0.55
26:4:36:GLU:HG3	42:n:53:VAL:CB	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:933:G:N1	27:A:1303:U:OP2	2.33	0.55
29:a:49:U:H2'	29:a:50:G:H8	1.71	0.55
29:a:1266:U:O2'	29:a:1267:U:OP1	2.25	0.55
33:e:132:VAL:HG11	33:e:177:VAL:HG21	1.88	0.55
39:k:73:LEU:C	39:k:74:ILE:HD13	2.32	0.55
26:4:37:VAL:CA	42:n:57:ARG:NH2	2.69	0.54
27:A:429:A:H2'	27:A:430:A:C8	2.42	0.54
29:a:928:A:H2'	29:a:929:G:H8	1.71	0.54
29:a:1295:U:O4	48:t:2:PRO:HD2	2.06	0.54
30:b:58:LYS:HA	50:c:16:PHE:CD2	2.42	0.54
3:G:103:PRO:HD2	3:G:106:MET:HE3	1.88	0.54
18:Z:49:VAL:HG22	18:Z:79:ASN:HB3	1.89	0.54
27:A:667:A:H4'	27:A:2724:U:H5'	1.88	0.54
27:A:800:A:N1	27:A:902:C:H1'	2.22	0.54
27:A:2261:U:H2'	27:A:2262:C:C6	2.42	0.54
27:A:2672:A:H5'	27:A:2673:U:H2'	1.89	0.54
29:a:87:G:H2'	29:a:88:G:H8	1.72	0.54
29:a:1375:G:N2	29:a:1486:A:H8	2.06	0.54
36:h:69:VAL:HG23	36:h:100:ALA:HB1	1.89	0.54
50:c:57:VAL:O	50:c:61:VAL:HG12	2.06	0.54
7:M:3:THR:HG22	13:T:64:ARG:NH1	2.22	0.54
27:A:857:U:H2'	27:A:858:A:H8	1.71	0.54
29:a:10:G:OP2	29:a:10:G:N2	2.41	0.54
29:a:294:C:OP1	29:a:590:A:O2'	2.23	0.54
29:a:481:G:OP1	41:m:114:ARG:NH2	2.40	0.54
29:a:768:U:O2'	51:w:97:GLU:HG2	2.07	0.54
29:a:1517:C:C5'	29:a:1518:A:H5'	2.36	0.54
32:d:62:ARG:NH1	32:d:64:ARG:HB2	2.22	0.54
47:s:17:THR:OG1	47:s:18:ARG:N	2.39	0.54
27:A:2088:C:H2'	27:A:2089:C:C5	2.42	0.54
29:a:1289:U:OP1	42:n:101:GLN:HG2	2.08	0.54
33:e:7:PRO:HB2	33:e:10:ARG:HG3	1.88	0.54
40:l:43:ILE:HG13	40:l:83:ALA:HB2	1.89	0.54
13:T:12:LYS:NZ	27:A:1342:C:OP1	2.31	0.54
27:A:844:G:O2'	27:A:878:G:H4'	2.08	0.54
27:A:2378:U:H2'	27:A:2379:G:H8	1.72	0.54
27:A:2901:G:H2'	27:A:2902:A:H8	1.72	0.54
29:a:1457:G:H2'	29:a:1458:G:C8	2.42	0.54
30:b:23:LEU:HA	30:b:26:ILE:HD12	1.90	0.54
42:n:19:LEU:HD13	42:n:33:ILE:HD11	1.90	0.54
8:N:48:PRO:HB3	29:a:1405:G:C5'	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:58:VAL:HG21	48:t:64:GLU:HG2	1.90	0.54
27:A:668:U:H2'	27:A:669:G:C8	2.43	0.54
29:a:1044:G:O2'	29:a:1171:G:N2	2.40	0.54
35:g:44:GLY:HA3	35:g:59:ILE:HG23	1.90	0.54
27:A:1076:A:H2'	27:A:1077:A:C8	2.43	0.54
29:a:82:U:O4	29:a:87:G:O6	2.25	0.54
29:a:910:G:OP1	51:w:113:HIS:HB2	2.05	0.54
29:a:1407:U:H2'	29:a:1408:A:H8	1.73	0.54
34:f:190:ALA:HB1	34:f:194:MET:HE2	1.90	0.54
17:X:24:LEU:HD12	17:X:25:VAL:HG23	1.90	0.54
27:A:138:A:H2'	27:A:139:U:O2	2.07	0.54
27:A:2065:A:H5'	29:a:682:A:C4'	2.38	0.54
27:A:3005:A:H5''	27:A:3006:G:H5'	1.88	0.54
28:B:116:C:H2'	28:B:117:A:C8	2.43	0.54
29:a:358:U:H2'	29:a:359:G:H8	1.73	0.54
29:a:452:A:H2	45:q:47:SER:CB	2.20	0.54
29:a:1305:G:H2'	29:a:1306:A:C8	2.43	0.54
43:o:32:ARG:NH1	43:o:48:LEU:HD22	2.22	0.54
44:p:6:GLU:H	44:p:6:GLU:CD	2.15	0.54
27:A:657:C:H2'	27:A:658:U:C6	2.43	0.54
27:A:1710:A:H62	27:A:1716:A:H8	1.56	0.54
29:a:858:A:H1'	37:i:12:THR:HG21	1.90	0.54
29:a:936:G:H21	29:a:1208:A:N6	2.02	0.54
29:a:1232:A:H62	29:a:1268:C:H42	0.69	0.54
40:l:118:THR:HA	51:w:220:ARG:HH21	1.72	0.54
43:o:32:ARG:HH21	48:t:7:LYS:HD3	1.73	0.54
51:w:136:ARG:HH21	51:w:254:THR:HG21	1.72	0.54
51:w:189:PRO:HD3	51:w:208:PRO:HB3	1.88	0.54
11:R:77:LYS:HB3	11:R:112:ARG:HD3	1.90	0.54
23:6:8:ARG:HA	23:6:27:LYS:O	2.08	0.54
27:A:339:U:H2'	27:A:340:A:C8	2.43	0.54
27:A:2070:A:H2'	27:A:2071:A:C8	2.43	0.54
27:A:2364:C:H2'	27:A:2365:A:C8	2.43	0.54
29:a:1220:A:H62	29:a:1281:A:N6	2.06	0.54
29:a:1296:C:H2'	29:a:1297:U:C6	2.43	0.54
27:A:190:A:H2'	27:A:191:G:N3	2.23	0.53
27:A:310:C:H2'	27:A:311:G:H8	1.73	0.53
27:A:997:G:H2'	27:A:998:G:C8	2.42	0.53
27:A:1099:A:OP2	27:A:1100:C:N4	2.42	0.53
28:B:50:C:H2'	28:B:51:G:H8	1.73	0.53
29:a:725:A:OP1	29:a:833:C:O2'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:975:G:O2'	29:a:976:A:N7	2.37	0.53
30:b:174:ILE:HD12	30:b:184:VAL:HG12	1.90	0.53
50:c:182:PRO:HD2	50:c:182:PRO:O	2.08	0.53
1:E:19:SER:HB2	1:E:204:ILE:HD11	1.89	0.53
4:H:20:ARG:HG2	4:H:35:ILE:HG21	1.89	0.53
24:7:7:THR:O	27:A:801:U:O2'	2.25	0.53
29:a:1197:U:OP1	43:o:3:LYS:HE3	2.07	0.53
29:a:1269:A:H2	29:a:1335:G:H1'	1.73	0.53
30:b:58:LYS:HD3	30:b:59:THR:HB	1.90	0.53
32:d:53:ASP:OD1	32:d:54:VAL:N	2.40	0.53
50:c:118:GLU:O	50:c:122:GLN:HG2	2.07	0.53
1:E:271:ARG:NH2	27:A:2016:G:OP2	2.41	0.53
4:H:57:ILE:HG13	4:H:91:PRO:HB2	1.90	0.53
27:A:1544:U:O4	27:A:1626:G:O6	2.26	0.53
27:A:1656:A:H2'	27:A:1657:G:H8	1.73	0.53
27:A:3020:U:O2'	27:A:3021:A:O5'	2.26	0.53
29:a:390:U:H2'	29:a:391:G:C8	2.43	0.53
38:j:33:LYS:HG3	38:j:33:LYS:O	2.08	0.53
1:E:26:ARG:HH22	1:E:30:GLU:HG2	1.73	0.53
3:G:4:LYS:HD2	3:G:17:SER:HB3	1.90	0.53
10:Q:95:THR:HG22	10:Q:115:LEU:HD23	1.89	0.53
27:A:1791:A:H2'	27:A:1792:A:C8	2.44	0.53
27:A:2086:U:H2'	27:A:2087:C:C6	2.44	0.53
27:A:2457:U:H2'	27:A:2458:G:H8	1.72	0.53
27:A:987:A:H2	27:A:1021:G:H22	1.55	0.53
27:A:1002:C:H2'	27:A:1003:A:H5''	1.91	0.53
27:A:1621:C:H2'	27:A:1622:G:H8	1.73	0.53
29:a:407:A:H2'	29:a:408:G:H8	1.73	0.53
29:a:544:C:OP2	41:m:12:ARG:NH2	2.25	0.53
29:a:1265:U:OP2	29:a:1266:U:O2'	2.17	0.53
33:e:189:PRO:O	33:e:190:LEU:HG	2.09	0.53
40:l:37:ASN:HA	40:l:67:SER:HB3	1.90	0.53
12:S:40:GLN:HG3	29:a:346:G:OP1	2.09	0.53
21:3:23:LEU:HD22	21:3:28:LEU:HD11	1.89	0.53
27:A:34:C:H2'	27:A:35:A:H8	1.72	0.53
27:A:928:U:H2'	27:A:929:C:C6	2.44	0.53
27:A:1501:C:H2'	27:A:1502:G:C8	2.43	0.53
29:a:163:G:H2'	29:a:164:G:H8	1.73	0.53
29:a:1040:U:O2'	39:k:54:SER:HB3	2.09	0.53
29:a:1508:C:H2'	29:a:1509:G:C8	2.43	0.53
35:g:8:VAL:HG22	35:g:61:ALA:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:c:44:GLN:OE1	50:c:44:GLN:N	2.40	0.53
13:T:6:ARG:HG2	27:A:1365:G:C5'	2.39	0.53
17:X:7:ASP:OD2	17:X:96:ARG:NH2	2.41	0.53
27:A:1690:A:H2'	27:A:1691:A:C8	2.43	0.53
27:A:2961:G:H2'	27:A:2962:A:C8	2.43	0.53
29:a:32:G:O2'	29:a:296:U:OP1	2.26	0.53
32:d:9:GLY:HA3	43:o:89:HIS:O	2.09	0.53
50:c:51:ASP:OD1	50:c:52:LYS:N	2.41	0.53
50:c:117:LEU:HB3	50:c:141:LYS:HE2	1.91	0.53
50:c:156:LYS:HD2	50:c:157:VAL:N	2.23	0.53
18:Z:14:ARG:NH2	27:A:2503:G:N7	2.56	0.53
27:A:1651:C:H2'	27:A:1652:A:C8	2.43	0.53
29:a:654:G:H21	40:l:127:HIS:HB2	1.74	0.53
29:a:1458:G:H2'	29:a:1459:G:O4'	2.08	0.53
38:j:88:ASP:OD1	38:j:88:ASP:N	2.41	0.53
51:w:133:ILE:HG22	51:w:250:TYR:HB2	1.91	0.53
7:M:56:VAL:HB	7:M:124:VAL:HG12	1.90	0.53
25:8:31:HIS:NE2	27:A:2616:A:OP2	2.31	0.53
27:A:1148:G:O6	27:A:1243:G:N2	2.42	0.53
43:o:45:VAL:O	43:o:49:GLN:HG3	2.09	0.53
51:w:126:ARG:HH21	51:w:249:HIS:CE1	2.27	0.53
2:F:151:ILE:HG12	27:A:2275:A:H4'	1.89	0.53
27:A:908:A:OP2	27:A:2294:A:O2'	2.26	0.53
27:A:1529:U:H3'	27:A:1530:G:H8	1.73	0.53
27:A:2387:U:H3'	27:A:2388:G:C8	2.44	0.53
27:A:2739:C:H2'	27:A:2740:G:H8	1.74	0.53
27:A:2854:A:N3	27:A:3112:A:O2'	2.39	0.53
29:a:1043:C:OP2	29:a:1044:G:O2'	2.25	0.53
29:a:1497:A:H2'	29:a:1498:C:C6	2.43	0.53
4:H:128:GLN:O	27:A:2527:G:O2'	2.27	0.52
9:O:131:GLY:O	9:O:135:GLU:HG2	2.09	0.52
27:A:296:A:N1	27:A:340:A:N6	2.57	0.52
28:B:5:C:OP1	28:B:62:C:O2'	2.26	0.52
29:a:895:A:H4'	29:a:896:A:O5'	2.09	0.52
29:a:1244:G:O6	29:a:1254:G:N2	2.41	0.52
30:b:91:LEU:HB2	30:b:101:ILE:HG22	1.91	0.52
24:7:6:ARG:HB2	27:A:1830:C:O2'	2.09	0.52
27:A:1970:G:N2	27:A:1973:C:OP2	2.37	0.52
29:a:1291:G:H8	42:n:99:ARG:HH21	1.54	0.52
51:w:161:HIS:CE1	51:w:163:PHE:HB3	2.41	0.52
26:4:57:ARG:HA	26:4:60:ARG:HG3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:564:G:N1	27:A:567:A:OP2	2.38	0.52
27:A:2088:C:H2'	27:A:2089:C:C6	2.45	0.52
27:A:2872:G:H2'	27:A:2873:U:C6	2.45	0.52
29:a:481:G:H2'	29:a:482:A:C8	2.44	0.52
29:a:504:G:H2'	29:a:505:C:C6	2.44	0.52
38:j:82:ASP:C	38:j:83:ILE:HD13	2.33	0.52
27:A:1020:A:H2'	27:A:1021:G:C8	2.45	0.52
27:A:1137:U:O2'	27:A:1139:A:N7	2.34	0.52
27:A:2216:G:N2	27:A:2220:C:O2'	2.42	0.52
29:a:498:C:H4'	29:a:499:C:O5'	2.10	0.52
29:a:1213:U:OP1	38:j:146:GLN:NE2	2.39	0.52
5:I:108:LEU:HD11	5:I:153:ARG:HB2	1.91	0.52
8:N:23:ARG:NH2	27:A:2772:G:N3	2.58	0.52
27:A:2131:G:O6	27:A:2148:C:N4	2.42	0.52
29:a:979:U:H2'	29:a:980:G:H8	1.75	0.52
39:k:7:ARG:HD2	39:k:73:LEU:HD11	1.90	0.52
25:8:33:LEU:HD23	25:8:36:LYS:HD2	1.92	0.52
27:A:2299:C:OP2	27:A:2462:G:N2	2.41	0.52
29:a:337:G:H2'	29:a:338:A:H8	1.75	0.52
29:a:1296:C:H2'	29:a:1297:U:H6	1.74	0.52
39:k:86:ALA:O	39:k:90:ILE:HG13	2.10	0.52
41:m:35:THR:N	41:m:54:ARG:O	2.43	0.52
51:w:10:GLU:OE1	51:w:10:GLU:N	2.42	0.52
20:2:62:ARG:NH1	20:2:65:GLU:OE1	2.43	0.52
27:A:89:A:O2'	27:A:90:C:OP1	2.25	0.52
27:A:639:C:O2'	27:A:640:G:H8	1.92	0.52
27:A:2901:G:H2'	27:A:2902:A:C8	2.44	0.52
29:a:45:G:H2'	29:a:46:G:H8	1.74	0.52
29:a:1168:G:P	38:j:135:LYS:CE	2.87	0.52
38:j:42:VAL:HG23	38:j:82:ASP:HB3	1.92	0.52
44:p:82:ILE:HG23	44:p:87:LEU:O	2.09	0.52
50:c:211:ALA:O	50:c:215:LYS:HG2	2.09	0.52
2:F:96:GLU:N	2:F:96:GLU:OE1	2.42	0.52
5:I:84:TYR:CZ	5:I:139:LYS:HB2	2.45	0.52
19:1:19:SER:HB2	27:A:2303:A:H5'	1.90	0.52
27:A:1001:C:C5	27:A:1002:C:H1'	2.44	0.52
27:A:1285:G:H2'	27:A:1286:C:C6	2.45	0.52
27:A:1790:A:H2'	27:A:1791:A:C8	2.44	0.52
27:A:2342:A:H61	27:A:2390:U:H1'	1.75	0.52
29:a:489:A:H8	29:a:523:U:O2'	1.93	0.52
29:a:1340:U:OP1	43:o:75:ARG:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1361:C:OP2	36:h:2:PRO:HB3	2.10	0.52
19:l:36:VAL:HG13	19:l:63:ARG:HE	1.75	0.52
26:4:36:GLU:C	42:n:54:THR:HG22	2.35	0.52
29:a:819:U:H3	29:a:829:G:H22	1.56	0.52
29:a:1425:G:H5''	29:a:1426:C:H5	1.74	0.52
26:4:64:ARG:HG2	48:t:5:LEU:CD2	2.40	0.52
27:A:137:G:H21	27:A:1524:G:H1'	1.74	0.52
27:A:929:C:H1'	27:A:1339:G:N2	2.24	0.52
27:A:994:A:H5''	27:A:1014:G:N2	2.25	0.52
27:A:2137:A:H2	29:a:1477:A:C8	2.28	0.52
27:A:2465:A:H2'	27:A:2466:G:C8	2.45	0.52
28:B:81:U:H2'	28:B:82:A:C8	2.44	0.52
29:a:60:U:H2'	29:a:61:G:H8	1.75	0.52
29:a:1040:U:H5''	39:k:53:ARG:HB3	1.91	0.52
29:a:1414:C:H2'	29:a:1415:G:O4'	2.10	0.52
29:a:1440:A:H3'	29:a:1441:G:H8	1.75	0.52
34:f:64:VAL:HG11	34:f:93:ARG:HG3	1.91	0.52
34:f:68:LYS:O	34:f:98:ARG:NH2	2.43	0.52
39:k:10:LEU:HB2	39:k:72:ARG:HB2	1.92	0.52
27:A:154:C:H2'	27:A:155:G:H8	1.73	0.51
27:A:2356:G:H2'	27:A:2380:G:H22	1.75	0.51
29:a:930:C:H2'	29:a:931:A:H8	1.75	0.51
29:a:1290:C:OP1	42:n:101:GLN:NE2	2.38	0.51
29:a:1509:G:OP1	40:l:131:ARG:NH2	2.43	0.51
34:f:135:ALA:HB1	34:f:162:VAL:HG23	1.92	0.51
50:c:108:HIS:O	50:c:112:GLN:HG2	2.10	0.51
17:X:75:ASP:OD2	17:X:100:THR:OG1	2.28	0.51
23:6:27:LYS:NZ	23:6:32:ASP:O	2.43	0.51
23:6:44:ASN:OD1	23:6:44:ASN:N	2.40	0.51
27:A:1087:G:H2'	27:A:1088:U:C6	2.45	0.51
27:A:1804:G:H2'	27:A:1805:G:C8	2.45	0.51
27:A:3057:U:H2'	27:A:3058:A:C8	2.45	0.51
29:a:666:U:H1'	40:l:53:TRP:NE1	2.16	0.51
29:a:926:G:N1	29:a:1320:G:OP2	2.43	0.51
18:Z:11:ARG:NH2	18:Z:12:ASN:OD1	2.44	0.51
27:A:1611:A:C2	35:g:17:ARG:CZ	2.84	0.51
29:a:1374:U:H2'	29:a:1375:G:C8	2.45	0.51
40:l:85:GLU:N	40:l:85:GLU:OE1	2.43	0.51
46:r:74:VAL:HG12	46:r:93:ILE:HG23	1.92	0.51
2:F:135:GLN:NE2	27:A:2802:G:H21	2.09	0.51
29:a:561:G:OP1	44:p:65:ARG:NH1	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:571:U:H2'	29:a:572:G:H8	1.75	0.51
29:a:964:U:H5''	43:o:6:LYS:CE	2.39	0.51
29:a:1486:A:H2	29:a:1489:G:H1	1.59	0.51
30:b:59:THR:HG21	30:b:99:ARG:HA	1.92	0.51
36:h:70:LYS:HG2	36:h:96:SER:HB2	1.93	0.51
36:h:113:GLU:HB2	36:h:119:ARG:HG2	1.93	0.51
37:i:22:HIS:O	37:i:66:TYR:OH	2.27	0.51
42:n:16:GLU:N	42:n:16:GLU:OE1	2.43	0.51
45:q:49:ILE:HB	45:q:93:LEU:HD11	1.92	0.51
50:c:97:LEU:H	50:c:100:MET:HE3	1.75	0.51
7:M:108:MET:HE2	27:A:1256:G:N2	2.26	0.51
27:A:1393:C:H2'	27:A:1394:A:H8	1.76	0.51
27:A:1523:U:H2'	27:A:1524:G:C8	2.46	0.51
27:A:2329:G:O6	27:A:2406:U:O4	2.28	0.51
29:a:890:A:H2'	29:a:891:A:C8	2.46	0.51
29:a:1337:A:H2'	29:a:1338:G:C8	2.45	0.51
43:o:32:ARG:HH12	43:o:48:LEU:HD22	1.76	0.51
50:c:44:GLN:HA	50:c:47:LEU:HD12	1.92	0.51
50:c:56:PHE:CG	50:c:198:TYR:HE2	2.29	0.51
3:G:23:GLU:OE2	3:G:23:GLU:N	2.27	0.51
4:H:40:LYS:HE2	4:H:164:VAL:HG11	1.93	0.51
27:A:310:C:H2'	27:A:311:G:C8	2.46	0.51
27:A:691:U:H2'	27:A:692:C:C6	2.46	0.51
27:A:728:G:H2'	27:A:729:C:C6	2.46	0.51
27:A:736:G:N2	27:A:738:A:H3'	2.25	0.51
27:A:1922:G:H2'	27:A:1923:G:H8	1.75	0.51
36:h:79:ARG:HG2	36:h:84:THR:HG23	1.93	0.51
43:o:19:ARG:O	43:o:23:ARG:NH1	2.44	0.51
2:F:154:CYS:N	27:A:2798:G:O2'	2.43	0.51
5:I:61:ARG:O	5:I:65:LEU:HD22	2.10	0.51
7:M:3:THR:HG22	13:T:64:ARG:HH12	1.76	0.51
13:T:83:LEU:HD22	13:T:88:VAL:HG11	1.92	0.51
27:A:608:C:H2'	27:A:609:G:H8	1.76	0.51
27:A:666:A:N6	27:A:2258:U:OP1	2.43	0.51
27:A:2363:A:H2'	27:A:2364:C:C6	2.46	0.51
27:A:2720:C:H2'	27:A:2721:A:O4'	2.11	0.51
29:a:1290:C:OP1	42:n:98:VAL:N	2.42	0.51
44:p:85:LEU:HB3	44:p:87:LEU:HG	1.91	0.51
27:A:242:G:O2'	27:A:254:G:O6	2.24	0.51
27:A:277:U:H2'	27:A:278:A:C8	2.46	0.51
27:A:640:G:O2'	27:A:642:G:OP2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1501:C:H2'	27:A:1502:G:H8	1.75	0.51
27:A:1621:C:H2'	27:A:1622:G:C8	2.46	0.51
27:A:2183:G:N3	29:a:1467:A:H2	2.08	0.51
27:A:2752:U:H3'	27:A:2754:G:C8	2.45	0.51
27:A:3014:A:O2'	27:A:3015:C:H5''	2.11	0.51
29:a:322:C:H2'	29:a:323:U:C6	2.46	0.51
29:a:719:C:OP1	35:g:2:ARG:NH2	2.39	0.51
36:h:109:ARG:HA	36:h:116:MET:HE1	1.93	0.51
7:M:36:LEU:HD11	7:M:122:LEU:HB2	1.93	0.51
21:3:5:LYS:HB2	21:3:59:VAL:HG22	1.93	0.51
26:4:34:VAL:HG12	42:n:50:ASP:CG	2.36	0.51
27:A:1479:G:H4'	27:A:2025:C:H5	1.75	0.51
27:A:2042:A:H2'	27:A:2043:C:C6	2.46	0.51
29:a:673:G:C8	51:w:96:TRP:CZ2	2.99	0.51
27:A:273:A:H62	27:A:313:G:N2	2.08	0.51
27:A:673:C:H2'	27:A:674:U:C6	2.46	0.51
27:A:2563:G:H2'	27:A:2564:A:H8	1.75	0.51
29:a:494:C:H2'	29:a:495:G:H8	1.76	0.51
51:w:242:ILE:HG12	51:w:252:LEU:HD13	1.92	0.51
27:A:1547:G:O6	27:A:1623:U:O4	2.28	0.50
27:A:1656:A:H2'	27:A:1657:G:C8	2.46	0.50
27:A:2467:U:H2'	27:A:2468:U:C6	2.46	0.50
29:a:83:U:C2	29:a:86:G:O6	2.63	0.50
29:a:413:G:O2'	29:a:428:G:N2	2.42	0.50
29:a:481:G:H2'	29:a:482:A:H8	1.75	0.50
29:a:1003:C:H2'	29:a:1004:G:C8	2.46	0.50
38:j:133:ARG:CG	43:o:101:TRP:NE1	2.71	0.50
23:6:9:PRO:HD2	23:6:27:LYS:O	2.11	0.50
27:A:678:A:N1	27:A:924:G:O2'	2.40	0.50
27:A:1073:G:O2'	27:A:1076:A:N6	2.44	0.50
27:A:2074:G:O6	27:A:2075:G:N1	2.45	0.50
29:a:399:G:H2'	29:a:400:C:C6	2.46	0.50
29:a:444:A:H2'	29:a:445:C:C6	2.45	0.50
29:a:832:U:H2'	29:a:833:C:C6	2.46	0.50
29:a:987:A:H2'	29:a:988:C:C6	2.46	0.50
29:a:1303:U:HO2'	48:t:78:ARG:NH2	2.05	0.50
33:e:197:GLU:OE1	34:f:137:ARG:NH2	2.26	0.50
36:h:116:MET:HE2	36:h:119:ARG:HE	1.76	0.50
48:t:22:GLN:HA	48:t:25:LYS:HZ2	1.76	0.50
3:G:61:GLY:HA3	3:G:80:ARG:HG2	1.93	0.50
27:A:880:G:H2'	27:A:881:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1025:A:N3	27:A:2488:C:O2'	2.41	0.50
27:A:1033:A:N3	28:B:81:U:O2'	2.40	0.50
27:A:1704:U:H2'	27:A:1705:C:C6	2.46	0.50
27:A:2366:C:H2'	27:A:2367:G:O4'	2.11	0.50
29:a:804:U:H2'	29:a:805:A:C8	2.46	0.50
29:a:1066:U:H3	29:a:1079:G:H22	1.58	0.50
29:a:1261:A:OP1	39:k:9:ARG:NH1	2.40	0.50
29:a:1342:A:N7	43:o:58:VAL:CG2	2.70	0.50
31:v:8:ARG:HA	31:v:11:ARG:HG2	1.94	0.50
50:c:42:ASP:HB3	50:c:45:GLN:OE1	2.11	0.50
51:w:146:VAL:HB	51:w:198:PHE:HB3	1.93	0.50
5:I:89:GLU:HA	5:I:131:LYS:HA	1.94	0.50
8:N:48:PRO:HB3	29:a:1405:G:H5''	1.93	0.50
27:A:971:G:H2'	27:A:972:A:C8	2.47	0.50
27:A:2686:U:H2'	27:A:2687:U:C6	2.47	0.50
27:A:2873:U:H2'	27:A:2874:C:C6	2.47	0.50
29:a:1384:G:OP1	51:w:84:ARG:NH2	2.45	0.50
27:A:815:G:O2'	27:A:1850:A:N3	2.38	0.50
27:A:1287:C:H2'	27:A:1288:A:H8	1.77	0.50
27:A:1373:A:H2'	27:A:1374:G:C8	2.47	0.50
27:A:1478:C:O2'	27:A:2026:A:N3	2.43	0.50
27:A:2386:U:OP1	27:A:2394:A:H5''	2.12	0.50
27:A:2850:C:H2'	27:A:2851:G:H8	1.76	0.50
29:a:298:A:H2'	29:a:299:G:C8	2.47	0.50
27:A:1233:A:H2'	27:A:1234:U:O4'	2.12	0.50
27:A:1907:A:H2'	27:A:1908:A:C8	2.46	0.50
27:A:2029:A:H2'	27:A:2030:C:C6	2.47	0.50
27:A:2752:U:H3'	27:A:2754:G:H8	1.76	0.50
29:a:194:A:N1	46:r:79:THR:OG1	2.37	0.50
51:w:51:PRO:HD2	51:w:72:VAL:HA	1.92	0.50
8:N:30:ARG:HG3	27:A:2898:G:H4'	1.93	0.50
14:U:47:ASN:N	14:U:47:ASN:OD1	2.41	0.50
26:4:60:ARG:NH1	29:a:1293:G:P	2.84	0.50
27:A:752:C:H2'	27:A:753:A:C8	2.47	0.50
27:A:1381:G:O2'	27:A:2236:G:O6	2.28	0.50
29:a:424:G:H2'	29:a:425:G:H8	1.77	0.50
2:F:157:PRO:HB2	2:F:159:ARG:HG3	1.94	0.50
23:6:37:GLU:OE1	23:6:52:LYS:NZ	2.45	0.50
24:7:13:ARG:HG3	27:A:122:A:C5	2.47	0.50
27:A:845:C:OP1	27:A:1992:U:O2'	2.23	0.50
27:A:2515:U:H2'	27:A:2516:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:10:G:O6	34:f:124:ALA:HA	2.11	0.50
29:a:407:A:H2'	29:a:408:G:C8	2.47	0.50
29:a:1128:C:O2	38:j:38:ARG:HD2	2.12	0.50
29:a:1337:A:H2'	29:a:1338:G:H8	1.76	0.50
2:F:27:THR:OG1	2:F:196:GLY:O	2.28	0.50
2:F:186:ASP:OD2	2:F:189:ASN:ND2	2.37	0.50
5:I:46:ALA:N	5:I:50:ALA:O	2.44	0.50
9:O:31:LYS:HE3	27:A:658:U:H5''	1.94	0.50
23:6:49:GLN:OE1	23:6:49:GLN:N	2.45	0.50
27:A:2:A:H2'	27:A:3:A:C8	2.47	0.50
27:A:151:A:H2'	27:A:152:G:C8	2.47	0.50
27:A:724:G:N2	27:A:727:A:OP2	2.32	0.50
27:A:2190:A:N3	27:A:2816:G:O2'	2.40	0.50
38:j:70:ALA:O	38:j:74:THR:HG22	2.12	0.50
41:m:50:ARG:NH1	41:m:89:ASP:OD2	2.43	0.50
27:A:130:C:H2'	27:A:131:A:H8	1.76	0.49
27:A:680:U:H2'	27:A:681:C:C6	2.46	0.49
27:A:681:C:H2'	27:A:682:A:C8	2.47	0.49
29:a:465:G:HO2'	29:a:466:U:H6	1.57	0.49
29:a:472:C:H2'	29:a:473:A:C8	2.47	0.49
29:a:507:G:O2'	29:a:515:A:N1	2.37	0.49
29:a:724:C:H2'	29:a:725:A:H8	1.77	0.49
29:a:1063:U:O2'	29:a:1082:A:OP2	2.25	0.49
29:a:1278:C:H4'	29:a:1284:U:O4	2.11	0.49
29:a:1298:G:N1	29:a:1301:A:OP2	2.42	0.49
35:g:30:ILE:HG22	35:g:71:THR:HG22	1.94	0.49
50:c:5:THR:OG1	50:c:6:MET:SD	2.69	0.49
29:a:587:A:OP1	29:a:611:G:N2	2.40	0.49
29:a:1110:A:H61	29:a:1125:G:H1'	1.78	0.49
29:a:1331:A:OP2	38:j:140:LYS:HE3	2.11	0.49
32:d:34:GLU:OE2	32:d:58:ARG:NE	2.45	0.49
39:k:26:VAL:HA	39:k:29:VAL:HG22	1.93	0.49
40:l:63:GLY:O	40:l:66:LYS:HG2	2.12	0.49
27:A:1091:A:H5'	27:A:1303:U:H1'	1.95	0.49
27:A:2157:G:C5'	31:v:26:VAL:HG21	2.42	0.49
27:A:3034:C:H2'	27:A:3035:C:C6	2.46	0.49
39:k:15:HIS:NE2	39:k:19:ASP:OD2	2.45	0.49
50:c:132:LYS:H	50:c:132:LYS:HD2	1.77	0.49
9:O:21:ARG:NH2	27:A:1365:G:N7	2.53	0.49
23:6:7:VAL:HG13	23:6:9:PRO:HD3	1.94	0.49
27:A:993:G:N1	27:A:1015:A:OP2	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1738:G:C2	27:A:1739:A:C8	3.00	0.49
29:a:25:G:H2'	29:a:26:G:H8	1.74	0.49
29:a:128:U:O2'	29:a:262:G:N3	2.44	0.49
33:e:166:LEU:HD23	33:e:177:VAL:HG22	1.94	0.49
3:G:6:ASP:OD1	3:G:6:ASP:N	2.38	0.49
27:A:502:C:H2'	27:A:503:A:H8	1.76	0.49
27:A:665:G:O2'	27:A:666:A:O5'	2.27	0.49
27:A:1296:G:H2'	27:A:1297:G:C8	2.48	0.49
27:A:2074:G:N2	27:A:2109:A:H62	2.10	0.49
27:A:2622:C:H2'	27:A:2623:A:H8	1.78	0.49
29:a:320:G:H2'	29:a:321:A:C8	2.47	0.49
32:d:28:TYR:HH	43:o:94:PRO:CD	1.97	0.49
40:l:110:GLN:O	51:w:207:HIS:NE2	2.42	0.49
1:E:72:LYS:NZ	1:E:99:ASP:OD2	2.45	0.49
4:H:143:SER:CB	42:n:3:ARG:NH1	2.67	0.49
11:R:118:ASP:O	11:R:122:GLU:HG3	2.13	0.49
27:A:2862:G:O2'	27:A:3002:A:N6	2.43	0.49
29:a:30:A:H61	29:a:538:G:H1'	1.78	0.49
29:a:203:U:H2'	29:a:204:A:C8	2.46	0.49
29:a:1295:U:H2'	29:a:1296:C:C6	2.47	0.49
51:w:177:GLY:H	51:w:182:TYR:HA	1.78	0.49
11:R:11:SER:HB2	28:B:31:C:H5'	1.94	0.49
27:A:1015:A:H2'	27:A:1016:C:O4'	2.12	0.49
27:A:2385:G:H5''	27:A:2394:A:H2'	1.93	0.49
27:A:2465:A:H2'	27:A:2466:G:H8	1.78	0.49
29:a:193:C:N3	46:r:20:ARG:HD2	2.27	0.49
32:d:64:ARG:NH2	32:d:66:ASP:OD2	2.43	0.49
39:k:88:MET:N	39:k:88:MET:SD	2.86	0.49
50:c:77:GLN:O	50:c:80:ILE:HG12	2.11	0.49
50:c:87:VAL:HG11	50:c:221:VAL:HG13	1.93	0.49
51:w:245:ARG:NE	51:w:249:HIS:HB2	2.26	0.49
1:E:37:LEU:HD13	1:E:62:TYR:HB2	1.93	0.49
13:T:66:ASN:ND2	27:A:1129:G:OP2	2.44	0.49
19:1:14:PHE:HZ	27:A:1480:A:N7	2.10	0.49
27:A:1052:U:H2'	27:A:1053:G:H8	1.77	0.49
29:a:1290:C:P	42:n:99:ARG:HG3	2.52	0.49
36:h:23:VAL:O	36:h:27:VAL:HG13	2.12	0.49
39:k:16:GLU:H	39:k:16:GLU:CD	2.19	0.49
5:I:126:VAL:HG22	5:I:132:PHE:HB2	1.95	0.49
7:M:104:ALA:O	7:M:108:MET:HG3	2.13	0.49
27:A:2297:U:H2'	27:A:2298:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2865:G:H2'	27:A:2866:A:H8	1.78	0.49
29:a:859:C:H2'	29:a:860:C:H6	1.78	0.49
40:l:73:GLN:HG3	40:l:108:SER:OG	2.13	0.49
4:H:126:PRO:O	4:H:174:ARG:NH1	2.36	0.49
12:S:38:ARG:CD	29:a:345:C:OP2	2.52	0.49
13:T:68:ALA:O	13:T:72:ASN:ND2	2.45	0.49
15:V:25:ARG:NH2	27:A:604:C:O2'	2.45	0.49
27:A:222:A:O2'	27:A:508:G:N3	2.36	0.49
27:A:610:C:O2	27:A:646:U:O2'	2.31	0.49
27:A:2387:U:H3'	27:A:2388:G:H8	1.78	0.49
29:a:663:G:N2	40:l:49:ASN:HA	2.27	0.49
36:h:57:ASP:OD1	36:h:59:VAL:N	2.44	0.49
47:s:51:ARG:NH1	47:s:56:ASN:O	2.43	0.49
4:H:83:GLN:OE1	4:H:83:GLN:N	2.46	0.48
27:A:586:U:H2'	27:A:587:G:O4'	2.13	0.48
27:A:735:U:H2'	27:A:736:G:O4'	2.13	0.48
27:A:2096:G:H2'	27:A:2097:G:H8	1.78	0.48
27:A:2351:A:H2'	27:A:2352:C:C6	2.49	0.48
27:A:2385:G:OP2	27:A:2387:U:N3	2.38	0.48
27:A:2443:U:H2'	27:A:2444:C:H6	1.78	0.48
29:a:449:C:O2	45:q:43:LYS:HE2	2.12	0.48
29:a:956:A:C2	43:o:71:ARG:NH1	2.80	0.48
32:d:129:PHE:HD2	32:d:133:MET:HE1	1.78	0.48
48:t:62:VAL:HA	48:t:66:MET:SD	2.53	0.48
6:J:1:MET:N	6:J:21:VAL:O	2.46	0.48
27:A:90:C:H2'	27:A:91:C:O4'	2.13	0.48
27:A:635:G:O2'	27:A:636:U:O4'	2.29	0.48
27:A:1537:U:H2'	27:A:1538:G:H8	1.78	0.48
27:A:2364:C:H2'	27:A:2365:A:H8	1.78	0.48
27:A:2673:U:H4'	27:A:2674:A:H5'	1.94	0.48
29:a:522:G:H2'	29:a:523:U:C6	2.48	0.48
29:a:863:G:OP2	41:m:6:GLN:NE2	2.35	0.48
29:a:1522:C:H6	29:a:1522:C:H5'	1.78	0.48
39:k:28:THR:HG21	39:k:90:ILE:HD11	1.94	0.48
40:l:28:GLY:HA2	40:l:46:PRO:HD3	1.94	0.48
7:M:71:LYS:NZ	27:A:1140:G:OP1	2.46	0.48
7:M:98:THR:HB	7:M:124:VAL:HG23	1.95	0.48
23:6:12:THR:HG21	23:6:21:ARG:HB3	1.95	0.48
27:A:32:G:H1'	27:A:542:A:C4	2.48	0.48
27:A:1554:U:H2'	27:A:1555:A:H8	1.78	0.48
27:A:1560:U:C2'	35:g:17:ARG:HD3	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:122:G:OP1	29:a:585:U:O2'	2.19	0.48
29:a:252:U:H2'	29:a:253:U:C6	2.48	0.48
29:a:805:A:H2'	29:a:806:C:C6	2.49	0.48
29:a:891:A:N3	29:a:1396:A:O2'	2.45	0.48
13:T:119:GLU:H	13:T:119:GLU:CD	2.20	0.48
27:A:726:A:H2'	27:A:727:A:C8	2.48	0.48
27:A:1314:C:H2'	27:A:1315:C:H6	1.78	0.48
27:A:1451:A:H2'	27:A:1452:G:C8	2.48	0.48
27:A:1560:U:H3	27:A:1611:A:H61	1.60	0.48
27:A:1620:U:H2'	27:A:1621:C:C6	2.48	0.48
27:A:1950:G:H2'	27:A:1951:G:H8	1.79	0.48
27:A:2249:G:H2'	27:A:2250:A:C8	2.48	0.48
29:a:299:G:H2'	29:a:300:A:C8	2.48	0.48
42:n:43:MET:HE2	42:n:47:ASP:HB2	1.96	0.48
27:A:264:G:H4'	27:A:516:G:H22	1.78	0.48
27:A:1537:U:H2'	27:A:1538:G:C8	2.48	0.48
27:A:1560:U:H2'	27:A:1561:C:O4'	2.13	0.48
27:A:2288:C:H2'	27:A:2289:C:H6	1.78	0.48
29:a:1517:C:H1'	51:w:111:TRP:HB3	1.94	0.48
30:b:164:TYR:HD1	30:b:167:LYS:HE2	1.78	0.48
31:v:27:GLN:HA	31:v:30:LYS:HD3	1.95	0.48
33:e:148:LEU:O	33:e:152:ILE:HG22	2.14	0.48
37:i:12:THR:HG22	37:i:15:ARG:HH12	1.78	0.48
45:q:54:GLU:H	45:q:54:GLU:CD	2.16	0.48
7:M:22:ASP:OD1	27:A:1260:C:N4	2.46	0.48
20:2:9:GLU:OE2	20:2:9:GLU:N	2.31	0.48
20:2:49:THR:O	20:2:53:GLU:HG3	2.14	0.48
27:A:159:A:OP2	27:A:164:A:N6	2.46	0.48
27:A:270:U:H1'	27:A:512:G:N2	2.28	0.48
27:A:1627:U:H2'	27:A:1628:A:H8	1.79	0.48
27:A:1705:C:H2'	27:A:1706:A:C8	2.47	0.48
27:A:2729:G:O2'	27:A:2730:U:O5'	2.30	0.48
29:a:498:C:H5''	29:a:499:C:C6	2.49	0.48
29:a:1281:A:H2'	29:a:1281:A:N3	2.29	0.48
29:a:1295:U:H2'	29:a:1296:C:H6	1.78	0.48
39:k:16:GLU:OE1	39:k:16:GLU:N	2.40	0.48
5:I:142:VAL:O	5:I:146:SER:OG	2.30	0.48
26:4:34:VAL:O	42:n:50:ASP:OD2	2.31	0.48
27:A:250:G:H2'	27:A:251:A:C8	2.49	0.48
27:A:2275:A:H8	27:A:2275:A:OP2	1.96	0.48
29:a:252:U:H2'	29:a:253:U:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:534:U:H2'	29:a:535:C:H6	1.79	0.48
32:d:177:THR:HG22	32:d:180:ALA:H	1.79	0.48
35:g:27:LEU:HD11	35:g:63:ILE:HD13	1.94	0.48
7:M:78:SER:HB3	27:A:2865:G:H5''	1.96	0.48
27:A:27:G:H2'	27:A:28:C:C6	2.49	0.48
27:A:81:A:N1	27:A:96:G:O2'	2.40	0.48
27:A:317:G:H2'	27:A:509:U:OP2	2.14	0.48
27:A:1719:C:C2	27:A:1720:G:C8	3.02	0.48
27:A:2439:C:H2'	27:A:2440:G:H8	1.78	0.48
27:A:2530:C:H5''	27:A:2531:G:H2'	1.96	0.48
29:a:175:A:OP1	49:u:56:ARG:NH2	2.47	0.48
29:a:674:G:H22	29:a:768:U:H5'	1.78	0.48
29:a:1265:U:H5''	29:a:1266:U:H4'	1.95	0.48
29:a:1516:U:O2'	51:w:111:TRP:HD1	1.97	0.48
2:F:69:GLN:NE2	27:A:3009:U:O2	2.47	0.48
9:O:37:THR:HG22	27:A:1060:U:OP1	2.14	0.48
14:U:61:THR:O	14:U:100:THR:OG1	2.30	0.48
17:X:42:LYS:HB3	17:X:59:ILE:HD11	1.96	0.48
27:A:672:C:H2'	27:A:673:C:C6	2.49	0.48
27:A:943:U:H4'	27:A:946:G:N1	2.29	0.48
27:A:979:G:H2'	27:A:980:C:C6	2.49	0.48
27:A:995:U:H2'	27:A:996:G:C8	2.48	0.48
29:a:269:U:H2'	29:a:270:A:H8	1.79	0.48
43:o:13:ARG:HG2	43:o:54:ASP:OD2	2.14	0.48
43:o:76:LYS:O	43:o:76:LYS:HD3	2.14	0.48
25:8:7:HIS:HB3	25:8:10:ALA:HB3	1.94	0.48
27:A:329:U:O2	27:A:446:G:C6	2.66	0.48
27:A:987:A:H2'	27:A:988:U:H5'	1.95	0.48
27:A:1544:U:C4	27:A:1626:G:O6	2.67	0.48
27:A:2086:U:O2	27:A:2096:G:N2	2.27	0.48
27:A:2800:G:O2'	27:A:2803:C:OP2	2.21	0.48
27:A:2883:G:N2	27:A:2885:G:H3'	2.29	0.48
29:a:81:C:H3'	29:a:82:U:H5''	1.95	0.48
29:a:263:A:H2'	29:a:264:U:C6	2.49	0.48
29:a:422:C:H4'	29:a:423:G:O5'	2.14	0.48
30:b:172:LYS:O	30:b:185:LEU:HD22	2.13	0.48
33:e:99:ARG:HA	33:e:99:ARG:HD3	1.74	0.48
34:f:87:LYS:O	34:f:90:GLU:HG3	2.13	0.48
44:p:87:LEU:O	44:p:88:ARG:C	2.57	0.48
46:r:77:MET:SD	46:r:89:ARG:NH2	2.86	0.48
27:A:139:U:H2'	27:A:140:G:O4'	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2750:G:H2'	27:A:2751:C:C6	2.49	0.47
28:B:10:G:O2'	28:B:11:U:H5'	2.14	0.47
29:a:425:G:H2'	29:a:426:U:C6	2.49	0.47
29:a:707:G:N2	29:a:710:G:OP2	2.40	0.47
30:b:148:LEU:HD22	30:b:153:VAL:HG22	1.96	0.47
39:k:47:ASN:O	39:k:66:GLU:HA	2.14	0.47
41:m:56:LYS:HE3	41:m:60:GLN:HA	1.96	0.47
42:n:80:ARG:HA	42:n:83:GLU:HG3	1.96	0.47
9:O:32:THR:HG22	9:O:35:ARG:H	1.79	0.47
17:X:24:LEU:HD11	17:X:34:LEU:HD23	1.95	0.47
26:4:64:ARG:HG2	48:t:5:LEU:HD21	1.96	0.47
27:A:750:C:H2'	27:A:751:A:C8	2.49	0.47
27:A:2729:G:H2'	27:A:2800:G:N1	2.29	0.47
29:a:1287:G:H22	29:a:1313:G:H1'	1.79	0.47
32:d:139:SER:O	32:d:142:ARG:NE	2.46	0.47
33:e:182:GLU:HB2	33:e:185:GLN:HE21	1.78	0.47
42:n:52:GLN:O	42:n:56:LEU:HD22	2.13	0.47
50:c:79:SER:O	50:c:83:GLU:HG2	2.14	0.47
2:F:154:CYS:SG	27:A:2796:A:H2'	2.54	0.47
5:I:39:GLU:CD	5:I:40:PRO:HD3	2.39	0.47
9:O:106:LYS:NZ	27:A:714:U:H1'	2.29	0.47
27:A:188:G:O6	27:A:204:G:O2'	2.29	0.47
27:A:587:G:N1	27:A:590:A:OP2	2.41	0.47
27:A:839:U:H2'	27:A:840:G:C8	2.49	0.47
27:A:947:U:H2'	27:A:948:G:C8	2.49	0.47
27:A:1122:C:H2'	27:A:1129:G:H2'	1.96	0.47
27:A:2147:U:H2'	27:A:2148:C:C6	2.48	0.47
27:A:2474:G:O2'	27:A:2720:C:OP1	2.23	0.47
27:A:2510:A:H4'	27:A:2511:A:O4'	2.14	0.47
27:A:2642:G:H2'	27:A:2643:U:O4'	2.14	0.47
27:A:2781:G:H2'	27:A:2782:C:C6	2.49	0.47
29:a:54:A:O2'	29:a:360:G:N2	2.47	0.47
40:l:102:ARG:O	40:l:106:ILE:HG13	2.14	0.47
42:n:12:ASP:OD1	42:n:44:ARG:NE	2.36	0.47
5:I:77:VAL:HA	5:I:80:VAL:HG22	1.96	0.47
9:O:63:LYS:NZ	27:A:249:C:O2	2.47	0.47
11:R:62:ALA:O	11:R:91:ARG:NH1	2.46	0.47
27:A:1003:A:OP1	27:A:1003:A:H2'	2.15	0.47
27:A:1297:G:H2'	27:A:1298:C:C6	2.49	0.47
27:A:1665:U:H2'	27:A:1666:A:H8	1.79	0.47
27:A:1758:G:H2'	27:A:1759:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2294:A:H2'	27:A:2295:C:C6	2.50	0.47
27:A:2304:C:H2'	27:A:2305:A:H8	1.79	0.47
27:A:2635:A:H2'	27:A:2636:A:C8	2.49	0.47
27:A:2678:G:N1	27:A:2723:C:N3	2.62	0.47
27:A:2849:G:H2'	27:A:2850:C:C6	2.49	0.47
27:A:2997:C:H2'	27:A:2998:C:H6	1.79	0.47
29:a:324:G:N1	29:a:327:A:OP2	2.48	0.47
33:e:98:TYR:O	33:e:160:ARG:NH2	2.47	0.47
37:i:76:GLY:HA3	37:i:132:TRP:CE2	2.49	0.47
39:k:22:ALA:O	39:k:26:VAL:HG12	2.15	0.47
1:E:247:VAL:HG12	1:E:253:PRO:HA	1.96	0.47
19:1:22:HIS:HB3	27:A:199:U:H4'	1.95	0.47
27:A:641:U:H5''	27:A:642:G:OP2	2.15	0.47
27:A:1373:A:H2'	27:A:1374:G:H8	1.78	0.47
27:A:1690:A:H2'	27:A:1691:A:H8	1.78	0.47
30:b:175:GLU:OE1	51:w:138:SER:HB2	2.15	0.47
41:m:18:LYS:HD3	41:m:18:LYS:HA	1.77	0.47
4:H:127:LYS:N	4:H:127:LYS:HD2	2.30	0.47
13:T:69:ALA:HB1	13:T:74:ILE:HG23	1.96	0.47
23:6:25:THR:HG21	27:A:2510:A:N6	2.29	0.47
27:A:2:A:H2'	27:A:3:A:H8	1.78	0.47
27:A:2363:A:N6	27:A:2375:G:O6	2.48	0.47
29:a:1094:C:H1'	43:o:100:SER:HB2	1.96	0.47
29:a:1169:A:OP1	38:j:136:TYR:HE1	1.96	0.47
33:e:47:ARG:NH1	33:e:51:GLN:OE1	2.47	0.47
35:g:4:TYR:CD2	35:g:72:VAL:HG21	2.49	0.47
46:r:83:SER:O	46:r:87:ARG:NH1	2.47	0.47
3:G:13:LYS:HE2	3:G:13:LYS:HB3	1.59	0.47
4:H:87:ARG:HB2	4:H:90:MET:HE1	1.97	0.47
7:M:45:THR:HG22	7:M:47:ASN:H	1.78	0.47
8:N:34:GLY:N	8:N:37:ASP:OD2	2.46	0.47
9:O:34:GLY:HA2	27:A:1305:G:H5''	1.97	0.47
11:R:21:ARG:HD3	27:A:2518:C:OP1	2.14	0.47
17:X:2:LYS:HB3	17:X:83:VAL:HG21	1.97	0.47
24:7:27:THR:HG23	24:7:30:GLY:H	1.79	0.47
26:4:61:PHE:CE2	48:t:41:ILE:CD1	2.98	0.47
27:A:665:G:N2	27:A:2255:A:OP1	2.47	0.47
27:A:729:C:O2'	27:A:733:U:OP1	2.33	0.47
27:A:2361:U:H3	27:A:2376:G:H22	1.62	0.47
27:A:2971:G:N2	27:A:2981:A:N6	2.23	0.47
29:a:805:A:H2'	29:a:806:C:H6	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1138:A:H1'	29:a:1162:G:N2	2.29	0.47
29:a:1203:G:OP2	29:a:1304:C:N4	2.43	0.47
32:d:151:VAL:HG22	32:d:200:VAL:HG22	1.96	0.47
33:e:80:LYS:HB2	34:f:127:GLY:HA3	1.97	0.47
4:H:64:LEU:HB2	4:H:72:PRO:HG3	1.97	0.47
7:M:72:LYS:HZ3	27:A:1257:G:H5'	1.80	0.47
17:X:37:GLY:HA2	17:X:40:ARG:NH2	2.27	0.47
26:4:37:VAL:CB	42:n:57:ARG:NH2	2.69	0.47
27:A:782:U:H2'	27:A:783:G:O4'	2.15	0.47
27:A:1313:U:H2'	27:A:1314:C:C6	2.50	0.47
27:A:2376:G:H2'	27:A:2377:G:H8	1.79	0.47
27:A:2603:G:H2'	27:A:2604:U:C6	2.50	0.47
29:a:518:U:H2'	29:a:519:A:H8	1.79	0.47
29:a:986:G:N2	29:a:987:A:N3	2.62	0.47
30:b:120:LYS:HE2	30:b:173:ILE:HG21	1.97	0.47
32:d:6:ASN:OD1	32:d:8:HIS:N	2.47	0.47
38:j:75:VAL:HG11	38:j:107:LEU:HD13	1.97	0.47
39:k:16:GLU:CD	39:k:16:GLU:N	2.73	0.47
39:k:45:GLU:HB3	39:k:69:THR:OG1	2.15	0.47
7:M:60:ASP:OD1	7:M:60:ASP:N	2.48	0.47
11:R:73:ILE:HG23	11:R:80:HIS:HD2	1.79	0.47
13:T:6:ARG:CZ	27:A:1366:A:C2	2.98	0.47
23:6:18:CYS:HB2	23:6:20:HIS:CE1	2.50	0.47
27:A:256:A:H2'	27:A:257:A:H8	1.80	0.47
27:A:1127:A:N3	27:A:1272:C:O2'	2.39	0.47
39:k:68:ARG:NH1	43:o:97:ARG:NH2	2.63	0.47
4:H:76:ARG:HH21	28:B:42:C:H42	1.61	0.47
4:H:99:ARG:HD2	28:B:44:C:O2'	2.15	0.47
7:M:136:GLN:HE21	27:A:3119:A:H5'	1.80	0.47
23:6:8:ARG:HG2	23:6:28:ASN:OD1	2.15	0.47
27:A:362:A:H2'	27:A:363:A:C8	2.50	0.47
27:A:502:C:H2'	27:A:503:A:C8	2.49	0.47
27:A:1487:U:O2'	27:A:2436:A:N3	2.42	0.47
29:a:688:C:C2	29:a:689:A:C8	3.03	0.47
29:a:1125:G:N2	29:a:1127:A:H62	2.13	0.47
29:a:1222:G:H2'	29:a:1223:G:H8	1.79	0.47
29:a:1409:A:H2'	29:a:1410:C:H6	1.80	0.47
39:k:7:ARG:NH1	39:k:75:ASP:OD2	2.48	0.47
42:n:91:ARG:HB3	42:n:98:VAL:HG12	1.95	0.47
1:E:99:ASP:O	27:A:1720:G:N2	2.48	0.46
1:E:221:VAL:HG21	27:A:897:A:N7	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:82:GLU:OE1	5:I:82:GLU:N	2.48	0.46
26:4:42:HIS:HB3	26:4:45:TYR:HD1	1.79	0.46
27:A:1223:U:H2'	27:A:1224:G:H8	1.80	0.46
27:A:1633:U:H2'	27:A:1634:C:C6	2.50	0.46
27:A:2400:C:H2'	27:A:2401:U:O4'	2.15	0.46
29:a:582:U:H2'	29:a:583:C:C6	2.50	0.46
29:a:905:A:O2'	29:a:1382:C:OP2	2.31	0.46
29:a:997:A:C2	29:a:1200:A:H1'	2.50	0.46
42:n:52:GLN:HA	42:n:55:VAL:HG12	1.97	0.46
46:r:63:ASP:OD1	46:r:63:ASP:N	2.48	0.46
1:E:181:GLU:HG3	1:E:271:ARG:HA	1.97	0.46
2:F:135:GLN:CD	27:A:2802:G:H21	2.22	0.46
5:I:90:ILE:HG12	5:I:130:THR:HA	1.96	0.46
6:J:10:GLU:CD	6:J:11:HIS:N	2.73	0.46
11:R:24:ARG:NH1	27:A:2518:C:OP2	2.47	0.46
19:1:49:ILE:HD11	19:1:61:VAL:HG23	1.98	0.46
26:4:13:THR:HB	26:4:32:THR:HG23	1.97	0.46
27:A:388:U:H2'	27:A:389:G:O4'	2.14	0.46
27:A:1434:G:H2'	27:A:1435:C:C6	2.50	0.46
27:A:1906:U:O2'	27:A:1918:A:N7	2.45	0.46
29:a:927:G:C2	29:a:928:A:C8	3.02	0.46
29:a:1084:G:OP1	50:c:110:ARG:NH1	2.48	0.46
38:j:61:ASN:O	38:j:65:GLN:HG3	2.15	0.46
39:k:12:ALA:HB2	39:k:96:VAL:HG22	1.97	0.46
51:w:183:ARG:HG3	51:w:203:THR:HG23	1.97	0.46
9:O:22:VAL:HG12	9:O:29:LYS:HD2	1.96	0.46
27:A:654:U:H1'	27:A:664:A:H1'	1.97	0.46
27:A:932:C:O2'	27:A:954:U:H5''	2.16	0.46
27:A:1437:A:N1	27:A:1448:C:O2'	2.41	0.46
27:A:1523:U:H2'	27:A:1524:G:H8	1.81	0.46
27:A:1608:U:H2'	27:A:1609:G:C8	2.50	0.46
29:a:481:G:H1'	29:a:529:C:H1'	1.96	0.46
29:a:604:U:O2'	45:q:11:GLY:HA2	2.15	0.46
29:a:858:A:H2'	29:a:859:C:C6	2.50	0.46
33:e:164:SER:OG	33:e:185:GLN:OE1	2.33	0.46
37:i:50:ARG:NE	37:i:52:GLU:OE2	2.48	0.46
38:j:76:ASP:OD1	38:j:76:ASP:O	2.33	0.46
40:l:39:THR:HG21	40:l:72:ALA:HB2	1.98	0.46
43:o:22:GLU:HB3	43:o:23:ARG:NH1	2.30	0.46
46:r:65:ASN:HB2	46:r:67:GLU:CD	2.40	0.46
27:A:282:A:C6	27:A:305:G:C6	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:875:G:H2'	27:A:876:A:O4'	2.16	0.46
27:A:1311:C:C2	27:A:1312:G:C8	3.04	0.46
27:A:1937:U:H2'	27:A:1938:G:O4'	2.15	0.46
29:a:191:C:H2'	29:a:192:G:O4'	2.15	0.46
29:a:230:G:H2'	29:a:231:G:O4'	2.15	0.46
29:a:673:G:C5	51:w:96:TRP:CE2	3.04	0.46
29:a:1221:U:C2	36:h:32:LEU:HD12	2.50	0.46
29:a:1301:A:C8	29:a:1305:G:C6	3.04	0.46
2:F:127:MET:HE2	2:F:146:ARG:HG2	1.98	0.46
5:I:98:GLN:HE22	5:I:100:LYS:HB2	1.81	0.46
27:A:1088:U:H2'	27:A:1089:C:C6	2.51	0.46
27:A:1614:G:H2'	27:A:1615:G:H8	1.81	0.46
27:A:1900:C:H2'	27:A:1901:C:C6	2.51	0.46
27:A:2471:A:H2'	27:A:2472:C:C6	2.50	0.46
29:a:382:A:H2'	29:a:383:A:C8	2.51	0.46
29:a:429:U:OP2	33:e:29:ARG:NH2	2.48	0.46
29:a:1237:C:H2'	29:a:1259:G:N7	2.30	0.46
42:n:33:ILE:HG13	42:n:34:LEU:N	2.30	0.46
43:o:22:GLU:HB3	43:o:23:ARG:NH2	2.31	0.46
48:t:22:GLN:HA	48:t:25:LYS:NZ	2.30	0.46
1:E:225:VAL:HG11	27:A:2005:C:H5''	1.97	0.46
2:F:104:GLU:H	2:F:104:GLU:CD	2.23	0.46
3:G:160:ARG:NH2	27:A:706:G:O2'	2.49	0.46
4:H:122:ARG:CD	42:n:72:ARG:CZ	2.86	0.46
21:3:40:ASN:O	21:3:44:ARG:HG2	2.16	0.46
27:A:402:G:H4'	27:A:404:A:N7	2.31	0.46
27:A:988:U:O2'	27:A:990:G:O4'	2.33	0.46
27:A:1314:C:H2'	27:A:1315:C:C6	2.50	0.46
27:A:1611:A:C6	27:A:1612:U:C4	3.03	0.46
27:A:1717:U:H5''	27:A:1718:C:H5	1.81	0.46
27:A:2329:G:N1	27:A:2406:U:N3	2.63	0.46
27:A:2401:U:H2'	27:A:2402:C:C6	2.51	0.46
27:A:2613:G:H5''	27:A:2614:U:O4'	2.16	0.46
27:A:2729:G:HO2'	27:A:2730:U:P	2.38	0.46
29:a:741:G:H2'	29:a:742:A:C8	2.50	0.46
29:a:741:G:H2'	29:a:742:A:H8	1.81	0.46
36:h:136:LYS:HE3	36:h:136:LYS:HB3	1.68	0.46
40:l:45:ASP:OD2	40:l:49:ASN:ND2	2.41	0.46
40:l:122:VAL:O	40:l:122:VAL:HG23	2.16	0.46
7:M:108:MET:HE2	27:A:1256:G:H21	1.80	0.46
22:5:7:ARG:NH1	27:A:671:G:O2'	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:722:G:H2'	27:A:723:C:C6	2.51	0.46
27:A:1332:G:C6	27:A:1347:G:C6	3.04	0.46
27:A:2857:A:H2'	27:A:2858:G:H8	1.80	0.46
29:a:36:A:H2'	29:a:37:A:C8	2.50	0.46
29:a:384:G:H2'	29:a:385:C:C6	2.51	0.46
29:a:667:A:C2	29:a:684:A:C5	3.04	0.46
29:a:823:U:O4	29:a:826:U:N3	2.44	0.46
29:a:1042:U:H2'	29:a:1043:C:C6	2.51	0.46
42:n:82:ILE:HA	42:n:89:GLY:HA2	1.98	0.46
44:p:85:LEU:C	44:p:87:LEU:H	2.24	0.46
50:c:225:LEU:O	50:c:228:ARG:HG2	2.16	0.46
8:N:24:VAL:HG13	8:N:33:ALA:HB2	1.96	0.46
13:T:6:ARG:HG2	27:A:1365:G:H5'	1.98	0.46
27:A:298:G:O2'	27:A:299:G:O4'	2.24	0.46
27:A:1529:U:H3'	27:A:1530:G:C8	2.50	0.46
27:A:1620:U:H2'	27:A:1621:C:H6	1.79	0.46
27:A:2098:U:H2'	27:A:2099:G:O4'	2.15	0.46
27:A:2761:U:H2'	27:A:2762:C:C6	2.50	0.46
29:a:664:U:H1'	40:l:49:ASN:HB3	1.97	0.46
29:a:1003:C:H2'	29:a:1004:G:H8	1.81	0.46
5:I:119:PRO:HD2	5:I:122:ILE:HD11	1.97	0.46
7:M:72:LYS:NZ	27:A:1257:G:H5''	2.31	0.46
27:A:154:C:H2'	27:A:155:G:C8	2.51	0.46
27:A:1659:U:H2'	27:A:1660:A:H8	1.79	0.46
27:A:2005:C:C2	27:A:2006:A:C8	3.03	0.46
27:A:2288:C:H2'	27:A:2289:C:C6	2.50	0.46
29:a:936:G:H2'	29:a:937:A:C8	2.51	0.46
29:a:1129:U:O5'	38:j:29:VAL:HG11	2.16	0.46
33:e:119:LEU:HD21	33:e:122:GLY:HA2	1.98	0.46
8:N:23:ARG:HB2	27:A:2785:A:O2'	2.16	0.46
27:A:265:A:N1	27:A:515:U:O2'	2.42	0.46
27:A:1430:C:H2'	27:A:1431:U:C6	2.51	0.46
27:A:1524:G:H2'	27:A:1525:U:C6	2.51	0.46
27:A:1541:G:OP2	27:A:1629:G:N2	2.49	0.46
27:A:1562:C:C4	27:A:1563:A:C8	3.05	0.46
27:A:2381:A:H4'	27:A:2382:G:O5'	2.16	0.46
27:A:2581:G:H2'	27:A:2583:C:OP2	2.15	0.46
27:A:2671:G:C8	27:A:2724:U:H3'	2.51	0.46
27:A:3055:G:H2'	27:A:3100:A:H61	1.81	0.46
29:a:337:G:H2'	29:a:338:A:C8	2.51	0.46
29:a:360:G:H2'	29:a:361:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1034:C:O2'	51:w:45:ASP:OD2	2.34	0.46
29:a:1218:C:O3'	29:a:1282:G:N2	2.47	0.46
38:j:114:ASP:OD1	38:j:114:ASP:N	2.30	0.46
45:q:82:LYS:HB2	45:q:89:ALA:HB2	1.97	0.46
50:c:9:LEU:O	50:c:12:SER:OG	2.34	0.46
9:O:80:VAL:HB	9:O:118:LEU:HD12	1.98	0.45
17:X:34:LEU:HD12	17:X:34:LEU:HA	1.85	0.45
23:6:37:GLU:OE2	23:6:37:GLU:HA	2.15	0.45
27:A:479:A:H1'	27:A:499:G:O4'	2.16	0.45
27:A:1762:C:H2'	27:A:1763:G:O4'	2.16	0.45
27:A:2443:U:H2'	27:A:2444:C:C6	2.51	0.45
28:B:11:U:O2'	28:B:12:C:H5'	2.16	0.45
28:B:50:C:H2'	28:B:51:G:C8	2.51	0.45
29:a:436:C:H2'	29:a:437:U:C6	2.52	0.45
29:a:493:A:H2'	29:a:494:C:C6	2.51	0.45
37:i:11:LEU:HD22	37:i:77:LEU:HD22	1.98	0.45
40:l:103:GLU:OE1	51:w:224:LEU:O	2.33	0.45
47:s:70:ASN:O	47:s:74:VAL:HG22	2.15	0.45
4:H:99:ARG:NE	28:B:44:C:O2	2.44	0.45
5:I:104:LEU:HG	5:I:106:PHE:HE1	1.82	0.45
14:U:28:ASP:OD1	14:U:28:ASP:N	2.42	0.45
20:2:14:THR:HG22	20:2:17:GLU:OE2	2.16	0.45
27:A:358:G:O5'	27:A:358:G:H8	1.99	0.45
27:A:502:C:H1'	27:A:2081:U:H1'	1.97	0.45
27:A:639:C:O2'	27:A:640:G:O5'	2.34	0.45
27:A:1259:U:H1'	27:A:1261:A:C6	2.51	0.45
27:A:1313:U:H2'	27:A:1314:C:H6	1.81	0.45
27:A:1652:A:H2'	27:A:1653:G:H8	1.82	0.45
27:A:2094:G:O2'	27:A:2095:G:H8	1.99	0.45
27:A:2421:A:O2'	27:A:2422:A:H8	1.99	0.45
28:B:40:A:C2	28:B:45:G:C2	3.04	0.45
29:a:431:A:C4	29:a:432:A:C8	3.04	0.45
29:a:1110:A:OP1	38:j:86:HIS:NE2	2.47	0.45
29:a:1299:C:H5'	43:o:48:LEU:HD21	1.95	0.45
29:a:1359:U:H2'	29:a:1360:A:C8	2.51	0.45
29:a:1432:C:H2'	29:a:1433:C:C6	2.51	0.45
41:m:5:GLN:HA	41:m:8:VAL:HG22	1.98	0.45
42:n:24:GLY:HA3	42:n:66:VAL:HG12	1.97	0.45
50:c:119:ALA:O	50:c:123:THR:HG23	2.16	0.45
50:c:203:ASN:OD1	50:c:204:ASP:N	2.50	0.45
2:F:94:GLU:OE1	2:F:94:GLU:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:154:VAL:HG23	3:G:193:ASP:HB2	1.98	0.45
27:A:265:A:N6	27:A:359:A:N7	2.64	0.45
27:A:294:G:O6	27:A:342:C:N4	2.43	0.45
27:A:506:C:H2'	27:A:507:G:H8	1.81	0.45
27:A:1288:A:H2'	27:A:1289:A:C8	2.51	0.45
29:a:246:A:C2	29:a:282:A:C5	3.05	0.45
29:a:279:A:OP1	29:a:280:C:O2'	2.32	0.45
29:a:335:C:H2'	29:a:336:A:H8	1.81	0.45
29:a:449:C:H2'	29:a:450:G:O4'	2.17	0.45
29:a:1110:A:H4'	38:j:40:ARG:NH1	2.30	0.45
38:j:26:ILE:HD12	38:j:26:ILE:O	2.17	0.45
51:w:4:ASP:OD1	51:w:4:ASP:N	2.38	0.45
2:F:52:LEU:HD11	2:F:84:LEU:HD22	1.99	0.45
27:A:664:A:H3'	27:A:665:G:C8	2.52	0.45
27:A:1154:G:C6	27:A:1238:G:C6	3.05	0.45
27:A:2096:G:H2'	27:A:2097:G:C8	2.51	0.45
29:a:264:U:O2'	46:r:81:PRO:O	2.32	0.45
29:a:606:U:OP1	45:q:19:ARG:NE	2.45	0.45
29:a:1076:C:H2'	29:a:1077:C:H6	1.82	0.45
30:b:47:ASP:OD1	30:b:48:ARG:N	2.49	0.45
30:b:131:ILE:HB	30:b:141:ASP:HB2	1.99	0.45
36:h:17:VAL:HG23	36:h:18:TYR:CD1	2.51	0.45
9:O:31:LYS:HD2	27:A:658:U:OP1	2.17	0.45
12:S:38:ARG:HH12	29:a:345:C:H3'	1.81	0.45
27:A:736:G:H1'	27:A:740:A:N6	2.32	0.45
27:A:1437:A:C2	27:A:1438:G:C8	3.04	0.45
27:A:1509:U:H2'	27:A:1510:A:O4'	2.17	0.45
27:A:2685:C:H2'	27:A:2686:U:C6	2.52	0.45
27:A:2815:C:H2'	27:A:2816:G:H8	1.82	0.45
29:a:270:A:H2'	29:a:271:C:C6	2.51	0.45
29:a:1232:A:H2'	29:a:1233:A:C8	2.52	0.45
36:h:40:GLU:OE2	38:j:63:VAL:HG21	2.17	0.45
48:t:16:LEU:O	48:t:19:VAL:HG22	2.17	0.45
17:X:86:ARG:HB3	17:X:97:ILE:HD13	1.98	0.45
27:A:183:G:H2'	27:A:184:C:C6	2.51	0.45
27:A:543:U:H3'	27:A:544:U:H5''	1.99	0.45
27:A:1236:G:H2'	27:A:1237:U:O4'	2.16	0.45
27:A:2065:A:H5'	29:a:682:A:H4'	1.98	0.45
27:A:2563:G:H2'	27:A:2564:A:C8	2.51	0.45
27:A:2609:A:H2'	27:A:2610:C:C6	2.52	0.45
27:A:2673:U:O3'	27:A:2674:A:H8	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:749:G:H4'	29:a:1497:A:H4'	1.97	0.45
29:a:902:U:H2'	29:a:903:U:C6	2.52	0.45
43:o:26:GLU:HA	43:o:29:ARG:HG3	1.98	0.45
45:q:108:ALA:O	45:q:112:GLU:HG3	2.17	0.45
20:2:15:ASP:O	20:2:19:LYS:HG2	2.16	0.45
27:A:49:A:OP2	27:A:114:G:N1	2.48	0.45
27:A:1287:C:H2'	27:A:1288:A:C8	2.52	0.45
27:A:1563:A:C6	27:A:1608:U:C4	3.05	0.45
27:A:2079:C:H2'	27:A:2080:G:H8	1.82	0.45
27:A:2439:C:H2'	27:A:2440:G:C8	2.52	0.45
27:A:2635:A:H2'	27:A:2636:A:H8	1.81	0.45
27:A:2759:G:H2'	27:A:2760:G:H8	1.82	0.45
27:A:2771:U:H2'	27:A:2772:G:H8	1.81	0.45
27:A:2920:U:H2'	27:A:2921:G:H8	1.81	0.45
29:a:581:U:H2'	29:a:582:U:C6	2.51	0.45
29:a:949:C:H4'	38:j:147:TYR:HE1	1.73	0.45
30:b:133:VAL:HG21	30:b:165:ILE:HG12	1.98	0.45
34:f:108:HIS:HD2	37:i:101:LEU:HD12	1.80	0.45
35:g:33:ASP:OD2	35:g:71:THR:OG1	2.31	0.45
40:l:92:ASP:HB2	40:l:118:THR:HG22	1.98	0.45
41:m:87:VAL:HG11	41:m:90:LEU:HD12	1.99	0.45
5:I:132:PHE:HZ	5:I:149:ILE:HG21	1.81	0.45
26:4:1:MET:HE2	26:4:6:HIS:CD2	2.51	0.45
27:A:1703:G:H2'	27:A:1704:U:C6	2.52	0.45
27:A:1875:U:H2'	27:A:1876:A:H8	1.82	0.45
29:a:23:C:H2'	29:a:24:U:C6	2.52	0.45
29:a:384:G:H2'	29:a:385:C:H6	1.81	0.45
29:a:522:G:H2'	29:a:523:U:H6	1.82	0.45
29:a:907:G:O2'	29:a:909:G:OP1	2.30	0.45
39:k:45:GLU:HB3	39:k:69:THR:HG1	1.82	0.45
40:l:90:LYS:HE2	40:l:90:LYS:HB3	1.73	0.45
51:w:175:TYR:CE1	51:w:183:ARG:HB3	2.52	0.45
21:3:13:ILE:HG12	27:A:1107:G:OP2	2.17	0.45
27:A:193:G:H2'	27:A:194:A:O4'	2.16	0.45
27:A:795:G:H2'	27:A:796:A:C8	2.51	0.45
29:a:1248:U:O2'	29:a:1249:G:O5'	2.34	0.45
29:a:1413:C:H2'	29:a:1414:C:C6	2.52	0.45
32:d:23:TYR:CE1	39:k:97:ASP:HB3	2.50	0.45
37:i:98:LEU:HD23	37:i:98:LEU:HA	1.85	0.45
48:t:17:LYS:O	48:t:21:VAL:HG13	2.16	0.45
50:c:223:GLU:O	50:c:226:GLN:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:w:195:LEU:HD12	51:w:196:SER:H	1.81	0.45
22:5:29:THR:HG22	27:A:3108:G:OP1	2.17	0.45
24:7:38:ARG:NE	27:A:50:A:H2	2.15	0.45
26:4:12:THR:HG21	26:4:26:SER:HB3	1.99	0.45
27:A:72:G:H2'	27:A:72:G:N3	2.32	0.45
27:A:660:U:N3	27:A:663:A:OP2	2.32	0.45
27:A:1284:A:H2'	27:A:1285:G:H8	1.82	0.45
27:A:2712:U:H2'	27:A:2713:G:C8	2.52	0.45
28:B:49:C:H2'	28:B:50:C:H6	1.82	0.45
29:a:321:A:H2'	29:a:322:C:H6	1.81	0.45
29:a:419:C:N3	29:a:425:G:N1	2.65	0.45
29:a:492:U:H2'	29:a:493:A:H8	1.81	0.45
29:a:1177:A:OP1	29:a:1178:A:H5''	2.16	0.45
29:a:1206:U:O2	29:a:1206:U:H2'	2.17	0.45
32:d:55:GLU:OE1	32:d:55:GLU:N	2.50	0.45
38:j:72:LEU:HA	38:j:75:VAL:HG12	1.98	0.45
43:o:12:GLN:O	43:o:15:GLU:HG3	2.17	0.45
1:E:52:ARG:NH2	27:A:2041:G:OP1	2.47	0.44
8:N:17:LYS:HB2	8:N:45:ASP:HB3	1.99	0.44
21:3:43:THR:O	21:3:47:ILE:HG23	2.17	0.44
27:A:392:A:C4	27:A:394:G:C8	3.05	0.44
27:A:1052:U:H2'	27:A:1053:G:C8	2.52	0.44
27:A:1086:C:H2'	27:A:1087:G:H8	1.82	0.44
27:A:2248:C:H2'	27:A:2249:G:C8	2.47	0.44
27:A:2751:C:H2'	27:A:2752:U:O4'	2.17	0.44
29:a:24:U:H2'	29:a:25:G:O4'	2.17	0.44
29:a:430:A:OP1	33:e:7:PRO:HA	2.17	0.44
29:a:463:C:OP2	29:a:464:G:O2'	2.34	0.44
29:a:1334:C:H2'	29:a:1335:G:C8	2.51	0.44
30:b:139:ILE:HG12	30:b:147:PHE:CD1	2.52	0.44
33:e:104:ARG:H	33:e:108:MET:CE	2.28	0.44
34:f:36:TYR:HD2	34:f:93:ARG:HH21	1.64	0.44
35:g:82:ASN:OD1	35:g:84:SER:OG	2.26	0.44
37:i:50:ARG:HH12	37:i:63:GLN:NE2	2.12	0.44
50:c:131:LYS:O	50:c:134:ILE:HG13	2.16	0.44
5:I:90:ILE:HG22	5:I:163:VAL:HG12	2.00	0.44
8:N:48:PRO:HB3	29:a:1405:G:H5'	2.00	0.44
24:7:21:PHE:HB2	24:7:46:THR:HG21	2.00	0.44
26:4:60:ARG:HH12	29:a:1293:G:P	2.40	0.44
27:A:412:A:O2'	27:A:413:G:N2	2.29	0.44
27:A:882:U:H2'	27:A:883:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1001:C:N4	27:A:1007:G:O6	2.50	0.44
27:A:1295:U:H2'	27:A:1296:G:H8	1.82	0.44
27:A:1675:U:O2'	27:A:1676:G:N7	2.50	0.44
27:A:1896:A:C4	27:A:1897:A:C8	3.05	0.44
27:A:2157:G:H5'	31:v:26:VAL:HG21	1.98	0.44
29:a:64:A:N7	29:a:104:A:H4'	2.31	0.44
29:a:620:A:H2'	29:a:621:U:C6	2.51	0.44
29:a:688:C:H2'	29:a:689:A:C8	2.51	0.44
29:a:725:A:H2'	29:a:726:G:C8	2.52	0.44
29:a:1249:G:H2'	29:a:1250:A:C8	2.52	0.44
37:i:101:LEU:HD23	37:i:101:LEU:HA	1.83	0.44
41:m:31:ARG:HE	41:m:31:ARG:HB3	1.62	0.44
43:o:64:ASP:OD1	43:o:79:LEU:HD23	2.17	0.44
17:X:77:ASP:OD1	17:X:77:ASP:N	2.34	0.44
25:8:34:GLU:OE1	25:8:35:HIS:N	2.50	0.44
27:A:546:G:O2'	27:A:557:G:O6	2.32	0.44
27:A:1560:U:N1	35:g:17:ARG:HD3	2.29	0.44
27:A:2343:G:H2'	27:A:2344:G:C8	2.52	0.44
27:A:2754:G:OP2	27:A:2759:G:N2	2.50	0.44
29:a:156:G:N2	29:a:159:A:OP2	2.44	0.44
29:a:542:U:H5''	29:a:543:A:C5	2.52	0.44
29:a:1393:G:H2'	29:a:1394:U:C6	2.52	0.44
37:i:10:PHE:CD2	37:i:36:ILE:HD11	2.48	0.44
41:m:54:ARG:HH11	41:m:64:THR:HB	1.82	0.44
50:c:68:LEU:HD22	50:c:70:VAL:HG23	2.00	0.44
3:G:108:ALA:HB1	3:G:112:ARG:NH1	2.32	0.44
8:N:110:LYS:HA	8:N:110:LYS:HD2	1.77	0.44
22:5:4:PRO:HG2	27:A:2240:U:O2	2.18	0.44
26:4:61:PHE:HZ	48:t:41:ILE:HD12	1.82	0.44
27:A:151:A:H2'	27:A:152:G:H8	1.80	0.44
27:A:316:U:O2'	27:A:317:G:OP1	2.29	0.44
27:A:722:G:H2'	27:A:723:C:H6	1.83	0.44
27:A:947:U:H2'	27:A:948:G:H8	1.80	0.44
27:A:1407:G:H2'	27:A:1408:C:C6	2.52	0.44
27:A:2450:C:C2	27:A:2451:A:C8	3.05	0.44
27:A:2604:U:H2'	27:A:2605:C:C6	2.53	0.44
27:A:2639:G:H2'	27:A:2640:G:H8	1.81	0.44
27:A:2897:G:H2'	27:A:2898:G:H8	1.81	0.44
29:a:534:U:H2'	29:a:535:C:C6	2.52	0.44
29:a:543:A:H2'	29:a:547:G:C8	2.53	0.44
29:a:1051:C:H2'	29:a:1052:G:C8	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1276:G:H2'	29:a:1277:U:C6	2.53	0.44
32:d:190:LYS:HG2	32:d:195:ARG:CZ	2.48	0.44
35:g:11:ASP:OD1	35:g:11:ASP:N	2.41	0.44
40:l:96:LYS:HD2	40:l:124:PRO:HD3	1.99	0.44
50:c:71:GLY:O	50:c:93:ASN:HA	2.18	0.44
5:I:104:LEU:HD21	5:I:132:PHE:CE2	2.50	0.44
18:Z:15:ASP:OD1	18:Z:16:SER:N	2.51	0.44
27:A:1815:G:H5'	27:A:1816:C:H5'	2.00	0.44
27:A:1854:U:H2'	27:A:1855:A:C8	2.52	0.44
27:A:2029:A:H2'	27:A:2030:C:H6	1.83	0.44
27:A:2070:A:H2'	27:A:2071:A:H8	1.81	0.44
29:a:826:U:H5'	29:a:827:U:OP1	2.16	0.44
30:b:114:GLY:HA2	30:b:117:GLU:OE1	2.18	0.44
51:w:131:ARG:HD3	51:w:248:GLY:O	2.17	0.44
19:l:45:ASN:OD1	19:l:45:ASN:N	2.49	0.44
27:A:55:G:H2'	27:A:56:U:C6	2.53	0.44
27:A:1400:G:N2	27:A:1443:G:H5'	2.32	0.44
27:A:1922:G:H2'	27:A:1923:G:C8	2.51	0.44
27:A:2343:G:H1	27:A:2401:U:H3	1.64	0.44
27:A:2375:G:H2'	27:A:2376:G:C8	2.53	0.44
27:A:2569:G:N3	27:A:2605:C:H2'	2.33	0.44
27:A:2678:G:H2'	27:A:2678:G:N3	2.33	0.44
27:A:2729:G:H2'	27:A:2800:G:C6	2.52	0.44
27:A:3018:U:H2'	27:A:3019:C:C6	2.53	0.44
29:a:26:G:H4'	29:a:867:G:C8	2.53	0.44
29:a:1239:G:H2'	29:a:1240:C:C6	2.53	0.44
51:w:126:ARG:HH21	51:w:249:HIS:HE1	1.65	0.44
51:w:222:GLY:HA2	51:w:244:ARG:NH2	2.33	0.44
12:S:48:ARG:HB2	12:S:95:LYS:HG2	1.99	0.44
18:Z:56:ASP:OD1	27:A:2588:C:H4'	2.18	0.44
26:4:36:GLU:CG	42:n:50:ASP:O	2.63	0.44
27:A:1296:G:H2'	27:A:1297:G:H8	1.81	0.44
27:A:1609:G:C2	27:A:1610:C:C2	3.05	0.44
29:a:109:G:H2'	29:a:110:U:C6	2.53	0.44
29:a:532:U:H2'	29:a:533:G:H8	1.83	0.44
29:a:1181:C:H4'	29:a:1182:A:H5'	2.00	0.44
32:d:90:LEU:HB3	32:d:98:VAL:HG11	2.00	0.44
14:U:39:VAL:HG12	14:U:55:LEU:HD22	2.00	0.44
20:2:56:ARG:O	20:2:60:VAL:HG23	2.18	0.44
27:A:671:G:C2	27:A:1377:A:C5	3.06	0.44
27:A:1223:U:H2'	27:A:1224:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1634:C:H2'	27:A:1635:A:C8	2.53	0.44
27:A:1678:U:H5'	27:A:1679:A:OP2	2.17	0.44
27:A:2084:A:H2'	27:A:2085:C:O4'	2.18	0.44
27:A:2279:C:N4	27:A:2724:U:H1'	2.33	0.44
27:A:2297:U:H2'	27:A:2298:U:H6	1.82	0.44
29:a:26:G:H2'	29:a:27:C:H6	1.83	0.44
29:a:375:U:H2'	29:a:376:G:H8	1.83	0.44
29:a:1167:G:O3'	38:j:135:LYS:CE	2.66	0.44
43:o:31:ILE:O	43:o:37:SER:OG	2.33	0.44
44:p:26:GLU:HG3	44:p:81:LEU:HD22	2.00	0.44
50:c:56:PHE:CD1	50:c:198:TYR:HE2	2.36	0.44
10:Q:8:PRO:HG2	27:A:1870:U:C4	2.53	0.44
27:A:277:U:H2'	27:A:278:A:H8	1.81	0.44
27:A:278:A:H2'	27:A:279:U:C6	2.52	0.44
27:A:1118:A:H2'	27:A:1119:A:C8	2.53	0.44
27:A:1412:C:H2'	27:A:1413:C:H6	1.82	0.44
27:A:1640:A:O2'	27:A:1641:U:OP1	2.35	0.44
27:A:1853:A:H2'	27:A:1854:U:O4'	2.18	0.44
27:A:2061:U:H2'	27:A:2062:G:H8	1.83	0.44
29:a:390:U:H2'	29:a:391:G:H8	1.82	0.44
29:a:789:G:OP2	44:p:48:HIS:CE1	2.70	0.44
29:a:1488:G:OP1	29:a:1491:A:H4'	2.18	0.44
50:c:61:VAL:HG13	50:c:224:GLY:HA3	1.99	0.44
50:c:84:ALA:O	50:c:88:GLY:N	2.48	0.44
1:E:155:LEU:HD13	1:E:177:MET:HE1	1.99	0.43
1:E:202:SER:HB3	27:A:2037:U:H1'	2.00	0.43
4:H:97:THR:OG1	28:B:43:C:N3	2.47	0.43
9:O:15:GLU:HB2	27:A:691:U:H4'	1.99	0.43
23:6:8:ARG:O	23:6:26:LYS:HD3	2.18	0.43
27:A:131:A:H2'	27:A:132:C:C6	2.53	0.43
27:A:190:A:H3'	27:A:191:G:H21	1.82	0.43
27:A:1611:A:H2'	27:A:1612:U:O4'	2.18	0.43
27:A:1645:G:H2'	27:A:1646:U:C6	2.53	0.43
27:A:1706:A:H2'	27:A:1707:G:H8	1.83	0.43
27:A:1714:A:H2'	27:A:1715:A:C8	2.53	0.43
29:a:96:G:C4	29:a:97:A:C8	3.06	0.43
29:a:653:G:H2'	29:a:654:G:H8	1.78	0.43
29:a:1514:G:H2'	29:a:1515:A:C8	2.53	0.43
46:r:81:PRO:HB3	46:r:87:ARG:CZ	2.47	0.43
51:w:147:ASP:O	51:w:151:LEU:HG	2.18	0.43
3:G:69:LYS:HZ2	27:A:2284:A:H5'	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3:13:ILE:HG21	27:A:1106:A:C5	2.52	0.43
27:A:621:U:H2'	27:A:622:C:C6	2.53	0.43
27:A:1716:A:H2'	27:A:1718:C:C5	2.53	0.43
27:A:1758:G:H2'	27:A:1759:A:C8	2.53	0.43
27:A:1849:G:N2	27:A:1852:A:OP2	2.40	0.43
27:A:2323:G:H2'	27:A:2324:A:C8	2.54	0.43
27:A:2329:G:O6	27:A:2406:U:C4	2.71	0.43
28:B:6:G:OP1	28:B:61:C:O2'	2.35	0.43
29:a:748:A:H4'	29:a:1507:G:H22	1.83	0.43
29:a:1011:U:O2'	29:a:1012:U:O5'	2.34	0.43
33:e:163:PRO:HG2	33:e:166:LEU:HD12	2.00	0.43
35:g:39:LYS:HE2	35:g:39:LYS:HB2	1.82	0.43
36:h:74:GLU:O	36:h:88:PRO:HA	2.18	0.43
36:h:111:ARG:NH2	36:h:113:GLU:OE2	2.52	0.43
48:t:10:PHE:HE2	48:t:37:ARG:HG3	1.83	0.43
48:t:45:ILE:HD13	48:t:45:ILE:HA	1.88	0.43
49:u:5:LYS:HB3	49:u:5:LYS:HE2	1.79	0.43
51:w:93:ALA:HB1	51:w:95:HIS:CD2	2.52	0.43
4:H:67:ILE:O	4:H:109:ARG:NH2	2.51	0.43
6:J:2:LYS:HA	6:J:2:LYS:HD3	1.77	0.43
27:A:303:G:H2'	27:A:304:U:O4'	2.19	0.43
27:A:632:G:H2'	27:A:633:A:C8	2.54	0.43
27:A:1630:U:H2'	27:A:1631:A:C8	2.53	0.43
27:A:1770:G:H2'	27:A:1771:U:C6	2.53	0.43
27:A:1939:U:H2'	27:A:1940:A:H8	1.82	0.43
27:A:1963:G:H2'	27:A:1964:U:C6	2.53	0.43
27:A:2692:A:P	27:A:2700:A:H61	2.41	0.43
29:a:45:G:H2'	29:a:46:G:C8	2.52	0.43
29:a:119:C:H2'	29:a:120:G:H8	1.83	0.43
29:a:493:A:H2'	29:a:494:C:H6	1.83	0.43
29:a:550:G:H2'	29:a:551:U:C6	2.53	0.43
29:a:953:G:H22	29:a:1346:A:P	2.40	0.43
30:b:172:LYS:HA	30:b:172:LYS:HD3	1.69	0.43
33:e:185:GLN:H	33:e:185:GLN:HG2	1.61	0.43
42:n:29:ARG:HD3	42:n:29:ARG:HA	1.59	0.43
44:p:18:HIS:NE2	44:p:21:ASP:HB3	2.33	0.43
50:c:131:LYS:HD3	50:c:134:ILE:HD11	2.00	0.43
2:F:87:ASP:OD1	2:F:88:ASP:N	2.51	0.43
2:F:88:ASP:C	2:F:88:ASP:OD1	2.60	0.43
27:A:363:A:H2'	27:A:364:A:O4'	2.19	0.43
27:A:990:G:O2'	27:A:991:C:OP2	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:994:A:H5''	27:A:1014:G:H21	1.84	0.43
27:A:1064:A:H2'	27:A:1065:C:C6	2.53	0.43
27:A:1393:C:H2'	27:A:1394:A:C8	2.52	0.43
27:A:1559:A:C4	27:A:1560:U:C5	3.05	0.43
27:A:1650:G:H2'	27:A:1651:C:C6	2.53	0.43
27:A:2170:U:H2'	27:A:2171:C:C6	2.53	0.43
27:A:2490:A:H4'	27:A:2491:A:N3	2.33	0.43
29:a:323:U:H2'	29:a:324:G:O4'	2.17	0.43
29:a:859:C:OP1	37:i:82:LYS:NZ	2.37	0.43
29:a:1099:C:H2'	29:a:1100:U:H6	1.83	0.43
33:e:90:GLU:O	33:e:95:ASN:ND2	2.52	0.43
38:j:47:GLN:HB3	38:j:82:ASP:OD2	2.19	0.43
38:j:47:GLN:NE2	38:j:48:PHE:O	2.51	0.43
38:j:48:PHE:CD2	38:j:55:LEU:HD22	2.53	0.43
40:l:30:ALA:HB3	40:l:93:VAL:HG22	2.01	0.43
43:o:38:PRO:HB2	43:o:41:ARG:HD3	1.99	0.43
48:t:19:VAL:HG21	48:t:44:PHE:CE1	2.50	0.43
49:u:35:PHE:CE1	49:u:51:LEU:HB2	2.53	0.43
51:w:126:ARG:CG	51:w:247:ASP:O	2.53	0.43
7:M:143:LYS:HE3	7:M:143:LYS:HB3	1.83	0.43
11:R:42:ARG:HG3	11:R:47:ILE:HD12	2.01	0.43
14:U:27:LEU:H	14:U:95:THR:HG21	1.83	0.43
17:X:8:THR:HG23	17:X:74:VAL:HG12	2.00	0.43
26:4:58:VAL:HG22	48:t:67:VAL:CG2	2.47	0.43
27:A:27:G:H2'	27:A:28:C:H6	1.83	0.43
27:A:214:G:H4'	27:A:215:A:H4'	2.00	0.43
27:A:460:G:O2'	27:A:488:G:O6	2.30	0.43
27:A:563:U:H4'	27:A:597:C:H5'	2.01	0.43
27:A:1907:A:H1'	29:a:1459:G:OP1	2.18	0.43
27:A:3014:A:N6	27:A:3112:A:H3'	2.33	0.43
27:A:3082:U:H2'	27:A:3083:A:H8	1.84	0.43
29:a:39:G:H2'	29:a:40:C:C6	2.54	0.43
29:a:573:U:C2	29:a:574:C:C5	3.07	0.43
29:a:658:U:H2'	29:a:659:C:H6	1.83	0.43
29:a:905:A:H2'	29:a:906:C:C6	2.53	0.43
29:a:1117:U:H4'	29:a:1118:A:OP1	2.18	0.43
29:a:1287:G:HO2'	29:a:1288:A:H8	1.63	0.43
51:w:131:ARG:HD2	51:w:250:TYR:OH	2.18	0.43
3:G:46:ARG:HB2	27:A:531:A:N7	2.34	0.43
7:M:108:MET:O	27:A:1124:C:O2'	2.23	0.43
12:S:33:GLU:O	12:S:36:LYS:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:X:82:ARG:NH2	27:A:382:A:OP2	2.49	0.43
27:A:9:U:O2	27:A:2850:C:H4'	2.18	0.43
27:A:543:U:H3'	27:A:544:U:C5'	2.49	0.43
27:A:858:A:O2'	27:A:1877:U:OP1	2.34	0.43
27:A:978:A:H2'	27:A:979:G:C8	2.53	0.43
27:A:2326:A:H2'	27:A:2327:C:C6	2.54	0.43
27:A:2441:G:H2'	27:A:2442:U:C6	2.54	0.43
27:A:2599:G:N2	27:A:2602:A:OP2	2.46	0.43
27:A:3059:G:C4	27:A:3060:A:C8	3.07	0.43
28:B:113:G:C2	28:B:114:A:C8	3.06	0.43
29:a:109:G:H1'	29:a:354:G:H5'	2.01	0.43
29:a:444:A:H2'	29:a:445:C:H6	1.82	0.43
29:a:657:U:O2	29:a:757:A:O2'	2.36	0.43
29:a:1098:U:H2'	29:a:1099:C:C6	2.54	0.43
29:a:1269:A:H2'	29:a:1270:A:C8	2.53	0.43
29:a:1369:G:H2'	29:a:1370:G:H8	1.83	0.43
33:e:23:ASP:OD1	33:e:25:SER:N	2.52	0.43
36:h:22:LEU:HD22	36:h:62:LEU:HD21	2.00	0.43
38:j:32:ARG:HD3	38:j:97:GLY:HA3	2.01	0.43
39:k:12:ALA:HB3	39:k:18:ILE:HD12	1.99	0.43
42:n:33:ILE:HD13	42:n:60:ILE:HD11	2.00	0.43
43:o:49:GLN:OE1	48:t:10:PHE:CD1	2.71	0.43
45:q:47:SER:O	45:q:49:ILE:HG13	2.18	0.43
1:E:217:LYS:HE3	1:E:217:LYS:HB3	1.72	0.43
10:Q:24:LEU:HB3	10:Q:44:LEU:HD22	2.00	0.43
13:T:4:VAL:HG11	27:A:1313:U:O2	2.18	0.43
14:U:53:ASP:OD1	14:U:54:ASP:N	2.51	0.43
15:V:52:GLU:HB2	15:V:53:PRO:HD3	1.99	0.43
23:6:18:CYS:HB2	23:6:20:HIS:NE2	2.33	0.43
27:A:781:C:H2'	27:A:782:U:C6	2.54	0.43
27:A:965:U:H2'	27:A:966:U:C6	2.54	0.43
27:A:1288:A:H2'	27:A:1289:A:H8	1.84	0.43
27:A:1535:C:H2'	27:A:1536:A:O4'	2.18	0.43
27:A:1630:U:H2'	27:A:1631:A:H8	1.84	0.43
27:A:2384:C:H5''	27:A:2387:U:O4	2.19	0.43
27:A:3086:U:OP2	27:A:3087:G:O2'	2.24	0.43
28:B:45:G:N2	28:B:49:C:C2	2.87	0.43
29:a:500:A:N6	29:a:509:G:H1'	2.33	0.43
29:a:1040:U:OP2	32:d:2:GLY:CA	2.62	0.43
29:a:1383:C:H1'	51:w:84:ARG:HD3	2.00	0.43
38:j:50:LEU:HD12	38:j:58:TYR:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:j:111:GLN:HG3	38:j:114:ASP:OD1	2.18	0.43
4:H:92:ILE:HD13	4:H:92:ILE:HA	1.94	0.43
5:I:12:PRO:HB2	5:I:15:VAL:HG12	2.00	0.43
5:I:35:LEU:HB2	5:I:76:LEU:HD13	2.01	0.43
5:I:147:ALA:O	5:I:151:ARG:HG3	2.19	0.43
13:T:53:ARG:NH1	27:A:1113:C:OP1	2.51	0.43
20:2:35:GLN:HB3	20:2:41:LEU:HD22	2.01	0.43
26:4:34:VAL:CG1	42:n:50:ASP:CB	2.97	0.43
27:A:301:U:C2	27:A:338:C:H5'	2.53	0.43
27:A:1515:C:N4	27:A:1516:G:O6	2.52	0.43
27:A:1530:G:H21	27:A:1805:G:N2	2.17	0.43
27:A:1560:U:H3'	27:A:1561:C:H6	1.82	0.43
27:A:1562:C:C2	27:A:1609:G:C2	3.06	0.43
27:A:1652:A:H2'	27:A:1653:G:C8	2.53	0.43
27:A:1733:C:H2'	27:A:1734:C:C6	2.53	0.43
29:a:846:A:H2'	29:a:847:A:C8	2.54	0.43
29:a:1098:U:H2'	29:a:1099:C:H6	1.84	0.43
30:b:144:LEU:HD13	30:b:181:ASN:HB3	2.00	0.43
34:f:50:VAL:HG22	34:f:51:LYS:H	1.84	0.43
37:i:5:ASP:OD2	37:i:79:ARG:NE	2.39	0.43
41:m:49:LEU:HD23	41:m:49:LEU:HA	1.85	0.43
1:E:80:ALA:O	1:E:113:GLN:NE2	2.49	0.43
4:H:57:ILE:O	4:H:61:ILE:HG12	2.18	0.43
20:2:66:LEU:HD23	20:2:66:LEU:HA	1.80	0.43
27:A:88:A:H1'	27:A:89:A:C8	2.53	0.43
27:A:263:G:O2'	27:A:517:A:N3	2.43	0.43
27:A:430:A:H2'	27:A:431:C:C6	2.54	0.43
27:A:619:C:H4'	27:A:620:G:C8	2.54	0.43
27:A:738:A:O2'	27:A:740:A:OP1	2.37	0.43
27:A:750:C:H2'	27:A:751:A:H8	1.84	0.43
27:A:1396:G:H2'	27:A:1397:U:H6	1.83	0.43
27:A:1611:A:C5	27:A:1612:U:C4	3.07	0.43
27:A:2074:G:H21	27:A:2109:A:N6	2.15	0.43
29:a:571:U:H2'	29:a:572:G:C8	2.54	0.43
29:a:1360:A:C2'	36:h:2:PRO:HG2	2.49	0.43
30:b:24:ALA:O	30:b:28:LYS:HG2	2.19	0.43
34:f:36:TYR:HE1	34:f:66:ASP:HB3	1.84	0.43
39:k:9:ARG:HB3	39:k:99:ASN:HB3	2.00	0.43
2:F:83:GLU:OE2	27:A:2859:C:O2'	2.37	0.43
15:V:48:GLN:O	15:V:51:SER:OG	2.36	0.43
26:4:34:VAL:CG1	42:n:50:ASP:HB2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:24:G:N2	27:A:599:G:H1'	2.34	0.43
27:A:646:U:H2'	27:A:647:G:O4'	2.19	0.43
27:A:977:G:H2'	27:A:978:A:O4'	2.18	0.43
27:A:1733:C:H2'	27:A:1734:C:H6	1.83	0.43
27:A:1907:A:H2'	27:A:1908:A:H8	1.84	0.43
27:A:2303:A:H2'	27:A:2304:C:C6	2.54	0.43
27:A:2394:A:H3'	27:A:2396:A:N7	2.34	0.43
27:A:2716:U:H2'	27:A:2717:U:H6	1.84	0.43
28:B:40:A:H2'	28:B:41:U:C6	2.54	0.43
29:a:492:U:H2'	29:a:493:A:C8	2.54	0.43
29:a:708:A:H2'	29:a:709:A:C8	2.54	0.43
29:a:832:U:H2'	29:a:833:C:H6	1.83	0.43
29:a:1168:G:O2'	38:j:133:ARG:NH1	2.51	0.43
29:a:1219:A:H2	29:a:1222:G:N3	2.16	0.43
30:b:33:PHE:O	30:b:34:ASN:OD1	2.37	0.43
32:d:104:GLU:O	32:d:106:LYS:NZ	2.52	0.43
38:j:29:VAL:HG12	38:j:38:ARG:HG2	2.01	0.43
39:k:72:ARG:HD3	39:k:72:ARG:HA	1.52	0.43
42:n:51:ASP:OD1	42:n:51:ASP:C	2.62	0.43
1:E:226:MET:SD	1:E:231:HIS:HB2	2.59	0.42
26:4:34:VAL:HG11	42:n:50:ASP:HB2	2.01	0.42
27:A:366:G:H2'	27:A:367:U:C6	2.54	0.42
27:A:663:A:N3	27:A:663:A:H2'	2.34	0.42
27:A:1822:C:O2'	27:A:1828:A:N1	2.43	0.42
27:A:2007:C:H2'	27:A:2008:A:C8	2.54	0.42
27:A:2265:U:H2'	27:A:2266:A:C8	2.54	0.42
27:A:2412:U:H2'	27:A:2413:G:C8	2.54	0.42
27:A:2777:G:C2	27:A:2807:G:H1'	2.55	0.42
29:a:580:G:C6	29:a:619:G:C6	3.07	0.42
29:a:725:A:H2'	29:a:726:G:H8	1.83	0.42
29:a:982:A:H2'	29:a:983:C:C6	2.54	0.42
40:l:91:VAL:O	40:l:117:GLY:N	2.31	0.42
40:l:106:ILE:HG13	40:l:106:ILE:H	1.70	0.42
50:c:74:LYS:HA	50:c:77:GLN:HB2	2.01	0.42
12:S:51:GLY:HA2	12:S:56:GLU:OE2	2.19	0.42
18:Z:39:ARG:NH2	27:A:2587:U:O2	2.50	0.42
27:A:804:A:H2'	27:A:805:C:C6	2.54	0.42
27:A:1089:C:O2'	27:A:1101:A:N3	2.47	0.42
27:A:2090:U:O2	27:A:2093:G:N2	2.52	0.42
27:A:3118:U:H2'	27:A:3119:A:C8	2.55	0.42
29:a:60:U:H2'	29:a:61:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:105:A:H5'	29:a:106:C:H5	1.84	0.42
29:a:426:U:H2'	29:a:427:U:C6	2.55	0.42
37:i:35:ASN:HB3	37:i:112:LEU:HD12	2.00	0.42
2:F:16:VAL:HG23	2:F:24:VAL:HB	2.01	0.42
9:O:59:MET:SD	27:A:250:G:H4'	2.59	0.42
10:Q:64:ARG:NH1	27:A:2930:G:O2'	2.52	0.42
13:T:9:ASN:OD1	27:A:1312:G:O2'	2.12	0.42
15:V:41:ASP:N	15:V:41:ASP:OD1	2.52	0.42
27:A:483:G:H2'	27:A:484:C:C6	2.54	0.42
27:A:844:G:H5'	27:A:845:C:H5''	2.02	0.42
27:A:978:A:H2'	27:A:979:G:H8	1.84	0.42
27:A:1435:C:C5	27:A:1444:U:H5''	2.55	0.42
27:A:1900:C:H2'	27:A:1901:C:H6	1.83	0.42
27:A:2249:G:H2'	27:A:2250:A:H8	1.84	0.42
27:A:2363:A:H2'	27:A:2364:C:H6	1.84	0.42
27:A:2457:U:H2'	27:A:2458:G:C8	2.51	0.42
27:A:2686:U:H2'	27:A:2687:U:H6	1.84	0.42
27:A:3070:G:H4'	27:A:3071:A:H5'	2.00	0.42
29:a:424:G:H2'	29:a:425:G:C8	2.54	0.42
29:a:1099:C:P	38:j:31:ARG:HH21	2.43	0.42
29:a:1104:G:N2	29:a:1105:U:O4	2.50	0.42
29:a:1116:U:O2'	29:a:1117:U:H5''	2.19	0.42
32:d:130:ARG:CZ	34:f:80:GLU:OE2	2.67	0.42
42:n:11:ARG:O	42:n:45:THR:OG1	2.36	0.42
51:w:175:TYR:CD2	51:w:228:PHE:HZ	2.37	0.42
3:G:31:ILE:HD11	9:O:4:ILE:HG12	2.02	0.42
24:7:9:GLN:O	27:A:801:U:C2	2.71	0.42
26:4:37:VAL:CA	42:n:57:ARG:HH12	2.32	0.42
26:4:60:ARG:CZ	29:a:1293:G:P	2.97	0.42
27:A:89:A:HO2'	27:A:90:C:P	2.41	0.42
27:A:130:C:H2'	27:A:131:A:C8	2.53	0.42
27:A:609:G:H2'	27:A:610:C:C6	2.54	0.42
27:A:824:G:H2'	27:A:825:C:C6	2.54	0.42
27:A:1076:A:O2'	27:A:2681:U:O2'	2.34	0.42
27:A:1076:A:HO2'	27:A:2681:U:HO2'	1.64	0.42
27:A:1412:C:H2'	27:A:1413:C:C6	2.54	0.42
27:A:1560:U:H3	27:A:1611:A:N6	2.17	0.42
27:A:2361:U:H3	27:A:2376:G:H1	1.66	0.42
27:A:2866:A:H2'	27:A:2867:A:H8	1.85	0.42
29:a:501:G:N7	41:m:50:ARG:NH2	2.64	0.42
29:a:606:U:OP2	45:q:19:ARG:NH2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:737:U:OP1	29:a:802:G:O2'	2.37	0.42
29:a:1086:G:H2'	29:a:1087:C:C6	2.54	0.42
30:b:116:ILE:HA	30:b:119:LEU:HD12	2.01	0.42
51:w:94:GLU:O	51:w:99:ARG:NH1	2.52	0.42
51:w:135:ARG:HB2	51:w:245:ARG:HD2	2.00	0.42
1:E:161:VAL:HG21	27:A:2036:A:H5''	2.01	0.42
2:F:13:MET:HG2	27:A:2906:U:C6	2.54	0.42
5:I:96:ARG:HH22	5:I:98:GLN:CG	2.31	0.42
5:I:104:LEU:HB3	5:I:116:ILE:HB	2.01	0.42
10:Q:7:GLY:O	10:Q:9:ARG:NH1	2.52	0.42
12:S:105:LYS:CE	29:a:1448:G:OP1	2.68	0.42
14:U:30:GLU:OE1	14:U:30:GLU:HA	2.19	0.42
24:7:9:GLN:O	27:A:801:U:O2	2.37	0.42
27:A:284:G:H1'	27:A:303:G:N1	2.34	0.42
27:A:733:U:H2'	27:A:734:C:C6	2.54	0.42
27:A:1271:C:H2'	27:A:1272:C:H6	1.83	0.42
27:A:1679:A:OP1	27:A:1679:A:H4'	2.20	0.42
27:A:1732:U:H2'	27:A:1733:C:H6	1.85	0.42
27:A:2336:U:O4	27:A:2337:A:N6	2.53	0.42
27:A:2480:G:H2'	27:A:2481:U:C6	2.54	0.42
27:A:2873:U:H2'	27:A:2874:C:H6	1.83	0.42
27:A:2887:G:H2'	27:A:2888:G:O4'	2.19	0.42
29:a:188:G:H2'	29:a:189:G:C8	2.55	0.42
29:a:800:U:H4'	29:a:801:G:OP2	2.20	0.42
29:a:1008:C:H2'	29:a:1009:C:C6	2.54	0.42
29:a:1035:A:C6	29:a:1187:G:C5	3.08	0.42
29:a:1382:C:C2	29:a:1486:A:N6	2.88	0.42
35:g:30:ILE:O	35:g:36:THR:OG1	2.30	0.42
42:n:15:MET:HE3	42:n:43:MET:SD	2.60	0.42
50:c:197:ASP:C	50:c:198:TYR:HD1	2.27	0.42
51:w:85:LEU:HD23	51:w:85:LEU:HA	1.86	0.42
1:E:53:HIS:HA	1:E:218:ARG:HB2	2.02	0.42
9:O:122:VAL:HG12	9:O:124:VAL:HG23	2.00	0.42
19:1:18:VAL:HG22	19:1:24:ARG:HG3	2.01	0.42
27:A:216:A:C4	27:A:217:G:C8	3.08	0.42
27:A:270:U:C2'	27:A:271:A:H5'	2.50	0.42
27:A:1150:A:H2	27:A:1240:G:H1	1.67	0.42
27:A:1939:U:H3	27:A:1955:A:H62	1.66	0.42
27:A:2074:G:H5'	27:A:2075:G:OP2	2.20	0.42
27:A:2338:G:O2'	27:A:2340:A:N7	2.37	0.42
27:A:3020:U:H1'	27:A:3022:G:O6	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:3116:C:H2'	27:A:3117:U:C6	2.55	0.42
28:B:63:U:H2'	28:B:64:G:H8	1.84	0.42
29:a:264:U:H2'	29:a:265:G:O4'	2.19	0.42
30:b:167:LYS:HD2	30:b:167:LYS:C	2.44	0.42
32:d:25:ASP:OD1	32:d:25:ASP:N	2.48	0.42
37:i:81:SER:OG	37:i:126:GLU:OE2	2.30	0.42
3:G:170:ARG:NH2	27:A:422:A:O2'	2.53	0.42
5:I:118:ALA:HB2	5:I:124:PHE:CE2	2.54	0.42
10:Q:65:GLU:O	10:Q:68:LYS:HG2	2.20	0.42
26:4:36:GLU:HA	42:n:54:THR:CG2	2.50	0.42
27:A:618:C:OP1	27:A:653:G:N2	2.48	0.42
27:A:747:A:H2'	27:A:748:U:O4'	2.19	0.42
27:A:869:U:H2'	27:A:870:G:H8	1.83	0.42
27:A:979:G:H2'	27:A:980:C:H6	1.85	0.42
27:A:1456:G:H8	27:A:1456:G:OP2	2.03	0.42
27:A:1534:C:H3'	27:A:1535:C:O2	2.19	0.42
27:A:1555:A:C2	27:A:1556:A:H1'	2.54	0.42
27:A:2357:A:N7	27:A:2379:G:N2	2.67	0.42
27:A:2460:U:H2'	27:A:2461:G:O4'	2.20	0.42
27:A:2717:U:C4	27:A:2718:G:C8	3.07	0.42
29:a:30:A:N6	29:a:538:G:H1'	2.34	0.42
29:a:144:G:H2'	29:a:145:G:H8	1.83	0.42
29:a:232:G:H1'	29:a:262:G:H1	1.85	0.42
29:a:988:C:O2'	29:a:1017:C:O2'	2.37	0.42
30:b:67:GLU:HB3	30:b:103:SER:HB2	2.02	0.42
30:b:173:ILE:HD12	30:b:183:VAL:CG2	2.50	0.42
47:s:18:ARG:C	47:s:19:LYS:HD2	2.45	0.42
5:I:151:ARG:NH2	27:A:2968:G:H1'	2.35	0.42
8:N:63:VAL:HG23	8:N:64:ARG:HG3	2.00	0.42
12:S:26:ASN:OD1	12:S:26:ASN:N	2.53	0.42
18:Z:11:ARG:O	18:Z:14:ARG:NH1	2.53	0.42
23:6:25:THR:HG22	23:6:26:LYS:N	2.35	0.42
26:4:36:GLU:O	42:n:54:THR:CG2	2.65	0.42
27:A:215:A:C8	27:A:520:A:N6	2.87	0.42
27:A:503:A:H2'	27:A:504:C:C6	2.54	0.42
27:A:737:A:N1	27:A:2593:A:O2'	2.50	0.42
27:A:1323:G:O2'	27:A:1352:A:N1	2.44	0.42
27:A:1732:U:H2'	27:A:1733:C:C6	2.55	0.42
27:A:1900:C:OP2	27:A:1917:G:N2	2.46	0.42
28:B:63:U:H2'	28:B:64:G:C8	2.55	0.42
28:B:81:U:H2'	28:B:82:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:136:G:C6	29:a:225:G:C5	3.07	0.42
29:a:581:U:H2'	29:a:582:U:H6	1.84	0.42
29:a:751:G:H2'	29:a:752:U:C6	2.54	0.42
29:a:1099:C:P	38:j:31:ARG:NH2	2.92	0.42
29:a:1123:G:C2	29:a:1124:G:H1'	2.55	0.42
29:a:1133:G:H4'	39:k:15:HIS:NE2	2.35	0.42
32:d:83:ALA:O	32:d:86:ILE:HG13	2.20	0.42
38:j:39:VAL:HG21	38:j:103:ILE:HD13	2.02	0.42
50:c:186:ILE:HG13	50:c:186:ILE:O	2.20	0.42
51:w:124:PHE:CD1	51:w:125:PRO:HD2	2.55	0.42
51:w:193:ASP:OD1	51:w:194:GLU:N	2.52	0.42
7:M:27:ARG:NH2	27:A:1260:C:O2'	2.29	0.42
9:O:133:ALA:O	9:O:137:ILE:HG13	2.20	0.42
17:X:22:LYS:HE3	17:X:22:LYS:HB2	1.89	0.42
27:A:72:G:H22	27:A:108:A:H2	1.66	0.42
27:A:1560:U:H1'	35:g:17:ARG:CG	2.48	0.42
27:A:2137:A:N3	29:a:1477:A:C6	2.87	0.42
27:A:2374:U:H2'	27:A:2375:G:H8	1.84	0.42
29:a:163:G:H2'	29:a:164:G:C8	2.55	0.42
29:a:824:C:O2'	29:a:826:U:O4	2.38	0.42
29:a:930:C:P	42:n:106:ASN:HB3	2.59	0.42
29:a:1249:G:O2'	29:a:1250:A:O4'	2.34	0.42
32:d:33:LYS:HE3	32:d:33:LYS:HB3	1.84	0.42
32:d:41:LEU:HD21	32:d:89:ASP:OD1	2.20	0.42
32:d:130:ARG:NH2	34:f:80:GLU:OE2	2.53	0.42
32:d:134:ARG:O	32:d:138:GLN:HG2	2.19	0.42
42:n:15:MET:HE2	42:n:15:MET:HA	2.01	0.42
44:p:34:LYS:NZ	44:p:38:ASP:OD1	2.53	0.42
46:r:69:GLY:H	46:r:96:LYS:NZ	2.18	0.42
50:c:5:THR:HG23	50:c:7:LYS:H	1.85	0.42
50:c:12:SER:HB3	50:c:208:ARG:HG2	2.01	0.42
16:W:55:ASP:OD1	16:W:55:ASP:C	2.62	0.42
27:A:189:A:N3	27:A:794:G:O2'	2.49	0.42
27:A:377:C:H2'	27:A:378:G:H8	1.84	0.42
27:A:465:A:C6	27:A:486:G:C6	3.08	0.42
27:A:751:A:H2'	27:A:752:C:C6	2.55	0.42
27:A:1155:C:H2'	27:A:1156:A:C8	2.55	0.42
27:A:2170:U:H2'	27:A:2171:C:H6	1.85	0.42
27:A:2340:A:H62	27:A:2388:G:H1	1.68	0.42
27:A:3024:A:H2'	27:A:3025:G:H8	1.85	0.42
28:B:92:G:H2'	28:B:93:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:320:G:HO2'	29:a:1418:G:HO2'	1.59	0.42
29:a:1279:U:H1'	29:a:1280:C:H5	1.85	0.42
29:a:1510:G:H2'	29:a:1511:C:C6	2.55	0.42
38:j:138:LEU:HB3	38:j:143:LYS:O	2.19	0.42
40:l:115:GLU:HA	40:l:115:GLU:OE1	2.20	0.42
50:c:101:LEU:HB3	50:c:179:LEU:HD12	2.02	0.42
1:E:141:VAL:HG13	1:E:162:SER:HB2	2.02	0.41
2:F:165:ARG:NH2	27:A:2737:G:OP2	2.46	0.41
3:G:169:VAL:HB	3:G:175:VAL:HG11	2.02	0.41
7:M:19:ASP:OD1	7:M:19:ASP:C	2.63	0.41
11:R:113:ILE:O	11:R:116:LEU:HD23	2.19	0.41
27:A:690:G:C6	27:A:776:G:C6	3.08	0.41
27:A:1146:A:OP2	27:A:1244:A:N6	2.30	0.41
27:A:1378:U:C4	27:A:1379:G:C6	3.08	0.41
27:A:1475:G:C6	27:A:1487:U:C2	3.07	0.41
27:A:1756:G:H1'	27:A:1758:G:C6	2.55	0.41
27:A:2262:C:H2'	27:A:2263:G:O4'	2.19	0.41
28:B:46:A:C4	28:B:47:A:C8	3.07	0.41
28:B:112:C:C2	28:B:113:G:C8	3.08	0.41
29:a:775:C:H2'	51:w:100:ARG:HH12	1.84	0.41
29:a:1005:G:C6	29:a:1006:U:O4	2.72	0.41
51:w:28:ARG:HD3	51:w:28:ARG:HA	1.88	0.41
1:E:36:PRO:HB3	27:A:1790:A:H5'	2.02	0.41
11:R:37:ARG:HA	11:R:101:VAL:HG23	2.02	0.41
16:W:52:VAL:HG21	16:W:86:LEU:HD13	2.02	0.41
24:7:45:LEU:HD12	24:7:45:LEU:HA	1.87	0.41
27:A:41:A:H2'	27:A:42:G:O4'	2.21	0.41
27:A:307:G:H2'	27:A:308:U:C6	2.55	0.41
27:A:818:U:H2'	27:A:819:G:O4'	2.20	0.41
27:A:966:U:H2'	27:A:967:G:H8	1.84	0.41
27:A:1001:C:C6	27:A:1002:C:H1'	2.55	0.41
27:A:1639:G:H5'	27:A:1640:A:OP1	2.20	0.41
27:A:1859:A:H2'	27:A:1860:G:O4'	2.20	0.41
27:A:1938:G:N1	27:A:1955:A:OP2	2.38	0.41
27:A:2011:U:H2'	27:A:2012:C:C6	2.55	0.41
27:A:2330:U:H3'	27:A:2331:U:C6	2.55	0.41
27:A:2738:U:H2'	27:A:2739:C:C6	2.56	0.41
29:a:487:C:H3'	29:a:488:C:H2'	2.02	0.41
29:a:523:U:H2'	29:a:524:C:C6	2.56	0.41
29:a:664:U:O2	40:l:50:VAL:HB	2.20	0.41
32:d:130:ARG:O	32:d:134:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:23:LEU:HD23	35:g:23:LEU:HA	1.91	0.41
38:j:72:LEU:HB3	38:j:78:VAL:HG12	2.02	0.41
39:k:42:LEU:HD21	39:k:73:LEU:HB2	2.02	0.41
44:p:70:VAL:HG12	44:p:78:TYR:HB2	2.02	0.41
4:h:119:ARG:CD	42:n:6:GLY:O	2.68	0.41
5:I:19:ILE:HG12	5:I:24:LEU:HG	2.01	0.41
5:I:46:ALA:H	5:I:51:ILE:HA	1.84	0.41
5:I:104:LEU:HD12	5:I:104:LEU:HA	1.90	0.41
7:M:65:SER:OG	27:A:1259:U:OP2	2.30	0.41
12:S:38:ARG:NH1	29:a:345:C:H3'	2.35	0.41
13:T:108:ALA:O	13:T:112:VAL:HG13	2.20	0.41
22:5:4:PRO:HA	27:A:2839:U:C2	2.55	0.41
27:A:37:U:C2	27:A:528:G:N2	2.88	0.41
27:A:369:G:C6	27:A:434:G:C6	3.09	0.41
27:A:661:U:H2'	27:A:662:G:C8	2.54	0.41
27:A:935:A:H4'	27:A:951:G:H22	1.83	0.41
27:A:1048:A:C6	27:A:1050:A:C8	3.08	0.41
27:A:1485:C:H2'	27:A:1486:G:O4'	2.20	0.41
27:A:2011:U:H2'	27:A:2012:C:H6	1.85	0.41
27:A:2588:C:H2'	27:A:2589:G:O4'	2.19	0.41
27:A:2801:A:O4'	27:A:2836:C:N4	2.53	0.41
29:a:597:G:H21	45:q:12:LYS:HE2	1.85	0.41
29:a:955:G:H2'	29:a:956:A:C2	2.56	0.41
29:a:1040:U:P	43:o:85:ARG:HH21	2.42	0.41
29:a:1156:G:H2'	29:a:1157:A:H8	1.85	0.41
33:e:186:ILE:HG22	33:e:188:VAL:HB	2.01	0.41
45:q:17:GLN:HE21	45:q:41:HIS:CD2	2.39	0.41
50:c:151:ILE:HG23	50:c:154:MET:HG3	2.03	0.41
51:w:222:GLY:HA2	51:w:244:ARG:HH21	1.84	0.41
11:R:14:ARG:NH1	28:B:48:C:P	2.89	0.41
11:R:41:ASN:ND2	28:B:7:G:O3'	2.54	0.41
16:W:10:ILE:HD13	16:W:10:ILE:HA	1.90	0.41
22:5:35:GLN:H	22:5:35:GLN:CD	2.27	0.41
27:A:183:G:H2'	27:A:184:C:H6	1.84	0.41
27:A:327:U:O2	27:A:449:G:N2	2.53	0.41
27:A:384:G:H2'	27:A:385:G:C8	2.50	0.41
27:A:729:C:H2'	27:A:730:G:O4'	2.19	0.41
27:A:991:C:H2'	27:A:992:C:C6	2.55	0.41
27:A:1789:A:H2'	27:A:1790:A:C8	2.55	0.41
27:A:1982:G:O6	27:A:2212:A:N6	2.53	0.41
27:A:1988:C:H2'	27:A:1989:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2376:G:H2'	27:A:2377:G:C8	2.55	0.41
28:B:107:A:H2'	28:B:108:C:C6	2.56	0.41
29:a:560:C:H2'	29:a:561:G:O4'	2.20	0.41
29:a:831:A:C6	29:a:832:U:C4	3.08	0.41
43:o:27:LEU:HD23	43:o:27:LEU:HA	1.90	0.41
50:c:15:HIS:HB3	50:c:43:LEU:HD21	2.02	0.41
1:E:66:ASP:OD2	1:E:103:ARG:NH1	2.53	0.41
3:G:141:ALA:HB1	3:G:169:VAL:HG12	2.01	0.41
4:H:37:GLY:H	4:H:166:THR:HB	1.85	0.41
5:I:30:LYS:HD2	5:I:30:LYS:HA	1.65	0.41
27:A:443:C:H2'	27:A:444:U:O4'	2.20	0.41
27:A:740:A:O2'	27:A:741:G:H8	2.03	0.41
27:A:1149:G:H2'	27:A:1150:A:C8	2.55	0.41
27:A:1153:U:H2'	27:A:1154:G:H8	1.85	0.41
27:A:2415:G:H2'	27:A:2416:C:C6	2.55	0.41
27:A:2623:A:H2'	27:A:2624:C:C6	2.55	0.41
27:A:2884:A:H3'	27:A:2885:G:C8	2.56	0.41
27:A:2952:U:H2'	27:A:2953:U:C6	2.56	0.41
29:a:309:G:H2'	29:a:310:G:H8	1.85	0.41
29:a:448:A:OP2	29:a:465:G:N2	2.36	0.41
29:a:535:C:H2'	29:a:536:C:H6	1.86	0.41
29:a:771:G:O6	29:a:772:A:N6	2.53	0.41
29:a:1253:U:H2'	29:a:1254:G:O4'	2.20	0.41
29:a:1409:A:H2'	29:a:1410:C:C6	2.54	0.41
33:e:105:THR:HG23	33:e:108:MET:H	1.85	0.41
48:t:36:ARG:NH1	48:t:52:HIS:O	2.53	0.41
7:M:78:SER:CB	27:A:2865:G:H5''	2.50	0.41
15:V:104:ARG:HH11	27:A:2237:A:H5'	1.85	0.41
27:A:838:G:C4	27:A:839:U:C5	3.08	0.41
27:A:1149:G:H2'	27:A:1150:A:H8	1.86	0.41
27:A:2323:G:N2	27:A:2412:U:O2	2.41	0.41
29:a:589:A:C5	29:a:590:A:C8	3.08	0.41
30:b:31:LYS:HD2	30:b:31:LYS:C	2.46	0.41
41:m:99:ARG:NH1	41:m:105:GLN:O	2.53	0.41
45:q:14:ARG:HD3	45:q:14:ARG:HA	1.91	0.41
45:q:21:ILE:HG22	45:q:36:VAL:HG22	2.02	0.41
51:w:174:LEU:HD23	51:w:175:TYR:N	2.36	0.41
1:E:117:ILE:HD13	1:E:117:ILE:HA	1.89	0.41
3:G:165:GLY:O	3:G:169:VAL:HG22	2.21	0.41
10:Q:33:ARG:NH2	10:Q:114:GLU:OE2	2.48	0.41
27:A:672:C:H2'	27:A:673:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1244:A:H4'	27:A:1245:U:O4'	2.20	0.41
27:A:1294:U:H2'	27:A:1295:U:C6	2.55	0.41
27:A:1378:U:H2'	27:A:1379:G:C8	2.56	0.41
27:A:1532:G:H2'	27:A:1533:U:C6	2.55	0.41
27:A:1556:A:N1	27:A:1615:G:C6	2.89	0.41
27:A:1888:C:H2'	27:A:1889:U:O4'	2.20	0.41
27:A:1897:A:H2	27:A:1981:U:O4'	2.04	0.41
27:A:2556:C:O2'	27:A:2559:A:O2'	2.37	0.41
29:a:215:U:H4'	29:a:216:U:H5'	2.02	0.41
29:a:231:G:H22	29:a:262:G:N2	2.18	0.41
29:a:437:U:H2'	29:a:438:U:O4'	2.21	0.41
29:a:788:C:H2'	29:a:789:G:O4'	2.20	0.41
29:a:1207:C:N4	42:n:104:LYS:HE3	2.36	0.41
32:d:68:HIS:CD2	32:d:103:LEU:HB2	2.56	0.41
32:d:178:LEU:HD23	32:d:178:LEU:HA	1.78	0.41
40:l:84:GLN:NE2	40:l:112:ALA:O	2.34	0.41
40:l:114:LEU:HD12	40:l:114:LEU:HA	1.84	0.41
50:c:45:GLN:O	50:c:49:TYR:CD2	2.73	0.41
51:w:141:MET:HE3	51:w:255:PRO:HA	2.02	0.41
14:U:43:VAL:HG22	14:U:48:VAL:HG22	2.02	0.41
15:V:104:ARG:NH1	27:A:2237:A:H5'	2.36	0.41
27:A:150:C:H2'	27:A:151:A:H8	1.85	0.41
27:A:187:G:H2'	27:A:188:G:O4'	2.20	0.41
27:A:298:G:H2'	27:A:299:G:C4	2.55	0.41
27:A:445:U:H1'	27:A:446:G:OP2	2.20	0.41
27:A:919:A:H5'	27:A:920:G:P	2.61	0.41
27:A:1000:C:H3'	27:A:1001:C:H5''	2.02	0.41
27:A:2151:A:H2'	27:A:2152:A:C8	2.56	0.41
27:A:2313:A:H2'	27:A:2314:U:C6	2.54	0.41
27:A:2342:A:C2	27:A:2392:A:H2'	2.56	0.41
27:A:2681:U:H2'	27:A:2682:G:C8	2.55	0.41
27:A:2936:C:OP1	27:A:2938:G:H4'	2.21	0.41
27:A:2945:A:C4	27:A:2946:G:C8	3.08	0.41
27:A:2964:A:H2'	27:A:2965:A:C8	2.55	0.41
29:a:588:A:C2	29:a:589:A:H1'	2.55	0.41
29:a:689:A:H2'	29:a:690:G:H8	1.85	0.41
29:a:1422:G:H2'	29:a:1423:U:C6	2.56	0.41
38:j:108:ILE:HD11	38:j:115:ARG:HB2	2.02	0.41
40:l:33:LYS:HE2	40:l:35:THR:HG22	2.02	0.41
40:l:45:ASP:O	40:l:48:GLY:N	2.51	0.41
42:n:15:MET:HE1	42:n:45:THR:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:n:69:ASP:OD1	42:n:70:LEU:N	2.53	0.41
50:c:27:MET:O	50:c:31:ILE:HG12	2.21	0.41
1:E:125:ILE:CG1	35:g:81:LEU:HD13	2.51	0.41
1:E:146:GLU:HB2	1:E:189:CYS:HB3	2.03	0.41
2:F:38:ARG:NH1	27:A:3008:C:O2'	2.53	0.41
4:H:40:LYS:HD2	4:H:99:ARG:NH2	2.36	0.41
7:M:112:ASN:HB3	27:A:650:G:OP1	2.21	0.41
11:R:113:ILE:HA	11:R:116:LEU:CD2	2.51	0.41
13:T:37:GLU:HG3	27:A:1367:G:O6	2.21	0.41
16:W:95:LEU:HG	20:2:34:PHE:CD2	2.56	0.41
17:X:1:MET:O	17:X:2:LYS:HB2	2.21	0.41
18:Z:18:ALA:CB	27:A:2495:G:H5''	2.50	0.41
24:7:21:PHE:CE2	27:A:114:G:H4'	2.55	0.41
26:4:37:VAL:CA	42:n:57:ARG:NH1	2.79	0.41
26:4:61:PHE:CD1	26:4:61:PHE:C	2.99	0.41
27:A:164:A:H2'	27:A:165:U:C6	2.56	0.41
27:A:263:G:H2'	27:A:264:G:O4'	2.21	0.41
27:A:308:U:H2'	27:A:309:G:C8	2.52	0.41
27:A:736:G:H1'	27:A:740:A:H61	1.86	0.41
27:A:826:G:H2'	27:A:827:G:H8	1.85	0.41
27:A:993:G:N2	27:A:1015:A:O5'	2.50	0.41
27:A:1146:A:N3	27:A:2710:G:O2'	2.43	0.41
27:A:1284:A:H2'	27:A:1285:G:C8	2.55	0.41
27:A:1407:G:H2'	27:A:1408:C:H6	1.85	0.41
27:A:1739:A:C4	27:A:1740:G:C8	3.09	0.41
27:A:1886:A:O2'	27:A:1892:G:N7	2.42	0.41
27:A:2334:U:H4'	27:A:2341:U:H1'	2.03	0.41
27:A:2486:U:H2'	27:A:2487:C:H6	1.86	0.41
27:A:2878:A:N1	27:A:2889:A:H5''	2.35	0.41
27:A:2955:G:H2'	27:A:2956:G:C8	2.56	0.41
28:B:24:G:H2'	28:B:25:G:C8	2.56	0.41
28:B:47:A:C5	28:B:48:C:C5	3.08	0.41
28:B:52:G:H2'	28:B:53:A:C8	2.56	0.41
29:a:148:A:C5	29:a:149:A:C8	3.09	0.41
29:a:960:A:C8	29:a:961:C:H5	2.38	0.41
29:a:1105:U:C2	29:a:1107:G:C8	3.09	0.41
29:a:1291:G:P	42:n:98:VAL:HG21	2.61	0.41
29:a:1329:G:O2'	29:a:1356:G:O6	2.31	0.41
30:b:171:ALA:HB3	30:b:185:LEU:HD11	2.02	0.41
31:v:16:LYS:HD2	31:v:16:LYS:HA	1.90	0.41
31:v:27:GLN:O	31:v:30:LYS:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:d:6:ASN:OD1	32:d:6:ASN:C	2.63	0.41
32:d:23:TYR:CZ	39:k:97:ASP:CB	3.01	0.41
32:d:130:ARG:NH2	34:f:80:GLU:OE1	2.54	0.41
37:i:54:ALA:HB2	37:i:59:SER:OG	2.21	0.41
38:j:32:ARG:HG2	38:j:94:GLY:HA2	2.03	0.41
39:k:36:VAL:HG12	39:k:38:GLY:H	1.85	0.41
50:c:69:PHE:HA	50:c:162:TRP:HD1	1.86	0.41
50:c:208:ARG:HE	50:c:208:ARG:HB2	1.58	0.41
1:E:233:HIS:NE2	1:E:246:PRO:HA	2.37	0.41
3:G:108:ALA:HB1	3:G:112:ARG:HH11	1.86	0.41
4:H:41:VAL:HG21	4:H:107:LEU:HD13	2.03	0.41
5:I:22:GLN:HE21	5:I:39:GLU:HA	1.85	0.41
13:T:4:VAL:HG22	27:A:1314:C:H1'	2.03	0.41
26:4:36:GLU:CA	42:n:54:THR:HG22	2.51	0.41
27:A:1040:U:H2'	27:A:1041:A:C8	2.56	0.41
27:A:1471:G:H2'	27:A:1472:C:C6	2.56	0.41
27:A:1532:G:N2	27:A:1804:G:C4	2.89	0.41
27:A:2137:A:C2	29:a:1477:A:C8	3.07	0.41
27:A:2363:A:C6	27:A:2375:G:C6	3.08	0.41
27:A:2961:G:H2'	27:A:2962:A:H8	1.86	0.41
29:a:149:A:C5	29:a:150:G:C8	3.09	0.41
29:a:731:U:H2'	29:a:732:G:O4'	2.20	0.41
29:a:743:G:H2'	29:a:744:C:C6	2.55	0.41
29:a:821:C:C5	29:a:822:U:C2	3.09	0.41
29:a:849:G:H2'	29:a:850:C:C6	2.56	0.41
30:b:50:GLU:OE2	30:b:62:VAL:HB	2.22	0.41
32:d:95:GLY:C	32:d:96:LYS:HG3	2.46	0.41
36:h:113:GLU:HB3	36:h:118:GLU:HG2	2.02	0.41
39:k:19:ASP:OD1	39:k:72:ARG:NH1	2.53	0.41
42:n:80:ARG:O	42:n:84:ILE:HG23	2.22	0.41
50:c:27:MET:HE2	50:c:27:MET:HB2	1.93	0.41
1:E:108:PRO:HB3	1:E:143:HIS:CE1	2.57	0.40
12:S:105:LYS:HB2	29:a:1415:G:OP1	2.21	0.40
14:U:77:LYS:NZ	27:A:1110:C:OP1	2.41	0.40
25:8:33:LEU:HD13	27:A:2643:U:OP2	2.21	0.40
27:A:1043:G:C4	27:A:1044:U:C5	3.09	0.40
27:A:1296:G:C2	27:A:1297:G:C5	3.09	0.40
27:A:2235:C:H2'	27:A:2236:G:O4'	2.21	0.40
27:A:2506:G:H4'	27:A:2613:G:O2'	2.21	0.40
27:A:2968:G:N7	27:A:2979:C:H1'	2.36	0.40
28:B:91:G:H2'	28:B:92:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:397:A:H5'	29:a:398:C:OP1	2.20	0.40
29:a:500:A:N1	29:a:516:C:H1'	2.36	0.40
29:a:1089:C:C2	29:a:1090:A:C8	3.09	0.40
29:a:1411:A:H2'	29:a:1412:C:C6	2.56	0.40
29:a:1504:G:OP2	31:v:11:ARG:NH2	2.54	0.40
34:f:36:TYR:CE1	34:f:66:ASP:HB3	2.56	0.40
45:q:69:PRO:O	45:q:73:LEU:HG	2.22	0.40
47:s:56:ASN:OD1	47:s:56:ASN:N	2.54	0.40
49:u:42:GLY:HA2	49:u:86:LEU:HD11	2.03	0.40
50:c:94:GLN:OE1	50:c:146:ARG:NE	2.47	0.40
3:G:206:SER:O	3:G:210:LYS:HB3	2.20	0.40
8:N:115:VAL:HG13	8:N:121:VAL:HG21	2.03	0.40
9:O:5:LYS:HA	9:O:5:LYS:HD2	1.82	0.40
9:O:65:LYS:CD	27:A:2640:G:H5''	2.49	0.40
9:O:80:VAL:HG22	9:O:114:GLY:HA2	2.02	0.40
15:V:17:VAL:HG12	15:V:19:VAL:HG22	2.03	0.40
23:6:10:LYS:HD2	27:A:2644:C:H5''	2.03	0.40
27:A:742:G:C2	27:A:743:G:N7	2.89	0.40
27:A:2398:C:H2'	27:A:2399:A:H8	1.85	0.40
29:a:363:A:C2	41:m:28:PRO:HD2	2.56	0.40
29:a:535:C:H2'	29:a:536:C:C6	2.56	0.40
29:a:1385:C:H2'	29:a:1386:C:O4'	2.21	0.40
30:b:116:ILE:HG22	30:b:120:LYS:HE3	2.03	0.40
32:d:37:ALA:O	32:d:40:LYS:HG2	2.21	0.40
34:f:101:LEU:HD11	34:f:145:VAL:HG22	2.03	0.40
35:g:16:GLU:HA	35:g:19:VAL:HG23	2.03	0.40
36:h:86:GLN:HB2	36:h:148:ASN:HD22	1.86	0.40
38:j:31:ARG:HG2	38:j:36:VAL:HG22	2.04	0.40
50:c:181:ILE:HD13	50:c:181:ILE:HA	1.91	0.40
1:E:250:TRP:CD2	27:A:2022:U:H5''	2.57	0.40
4:H:182:PHE:HA	4:H:183:PRO:HD3	1.89	0.40
5:I:87:LYS:HD3	5:I:133:SER:OG	2.21	0.40
10:Q:78:THR:O	10:Q:82:GLU:HG2	2.21	0.40
15:V:100:ALA:HB2	27:A:1832:A:C2	2.56	0.40
27:A:883:G:H22	27:A:1494:U:H1'	1.86	0.40
27:A:1472:C:H2'	27:A:1473:G:O4'	2.22	0.40
27:A:1608:U:C6	27:A:1608:U:H5''	2.56	0.40
27:A:2622:C:H2'	27:A:2623:A:C8	2.55	0.40
27:A:2771:U:H2'	27:A:2772:G:C8	2.55	0.40
27:A:2857:A:H2'	27:A:2858:G:C8	2.57	0.40
27:A:2879:G:H22	27:A:2888:G:H3'	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B:78:U:H2'	28:B:79:A:H8	1.87	0.40
29:a:212:G:H2'	29:a:213:C:H6	1.85	0.40
29:a:673:G:N7	51:w:96:TRP:CZ2	2.90	0.40
38:j:37:VAL:HG11	38:j:99:LEU:HD13	2.03	0.40
39:k:80:THR:O	39:k:84:VAL:HG23	2.21	0.40
41:m:83:ARG:HB3	41:m:98:ILE:HD11	2.04	0.40
43:o:38:PRO:HB2	43:o:41:ARG:CD	2.51	0.40
49:u:35:PHE:CD2	49:u:79:LEU:HD22	2.56	0.40
51:w:165:GLU:HB3	51:w:168:THR:OG1	2.22	0.40
5:I:22:GLN:NE2	5:I:38:ALA:O	2.54	0.40
6:J:33:ARG:HG3	6:J:35:LEU:HG	2.03	0.40
11:R:31:GLY:N	11:R:54:ASP:OD2	2.34	0.40
11:R:87:LEU:HD12	11:R:87:LEU:HA	1.94	0.40
27:A:400:C:H2'	27:A:401:C:H6	1.87	0.40
27:A:600:A:H2'	27:A:601:A:H8	1.86	0.40
27:A:829:U:H5	44:p:88:ARG:CZ	2.35	0.40
27:A:1121:G:H2'	27:A:1122:C:C6	2.57	0.40
27:A:2305:A:C4	27:A:2463:G:N2	2.89	0.40
27:A:3030:A:H2'	27:A:3031:A:C8	2.57	0.40
28:B:25:G:N7	28:B:57:U:H2'	2.36	0.40
29:a:106:C:H2'	29:a:107:G:O4'	2.22	0.40
29:a:120:G:H2'	29:a:121:U:C6	2.56	0.40
29:a:619:G:C2	29:a:620:A:C8	3.10	0.40
29:a:1000:U:H2'	29:a:1001:G:C8	2.56	0.40
29:a:1185:A:H2'	29:a:1186:U:O4'	2.21	0.40
29:a:1473:A:H2'	29:a:1474:C:C6	2.57	0.40
29:a:1486:A:H2	29:a:1489:G:N1	2.20	0.40
32:d:188:GLU:HB3	32:d:195:ARG:HD2	2.02	0.40
33:e:138:ILE:HB	33:e:175:ILE:HB	2.03	0.40
43:o:16:LEU:HD22	43:o:19:ARG:HH12	1.85	0.40
50:c:129:ARG:HD2	50:c:133:GLU:CD	2.46	0.40
51:w:195:LEU:HD12	51:w:196:SER:N	2.36	0.40
51:w:230:PHE:HE1	51:w:239:ALA:HB1	1.87	0.40
1:E:177:MET:HE2	1:E:183:ARG:HB3	2.03	0.40
4:H:22:ALA:HA	4:H:25:GLN:HE21	1.86	0.40
5:I:149:ILE:O	5:I:152:LEU:HD23	2.21	0.40
6:J:10:GLU:CD	6:J:11:HIS:H	2.28	0.40
26:4:13:THR:HA	26:4:22:PHE:O	2.21	0.40
27:A:5:U:C2	27:A:6:G:C8	3.09	0.40
27:A:216:A:H2'	27:A:217:G:H8	1.87	0.40
27:A:691:U:H2'	27:A:692:C:H6	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1008:G:C2	27:A:1009:U:C4	3.09	0.40
27:A:1285:G:H2'	27:A:1286:C:H6	1.84	0.40
27:A:1560:U:C5	27:A:1561:C:C4	3.10	0.40
27:A:1848:A:N6	27:A:1855:A:N6	2.69	0.40
27:A:2137:A:N3	29:a:1477:A:C2	2.90	0.40
27:A:2548:U:H5''	27:A:2549:G:H5''	2.03	0.40
27:A:2815:C:H2'	27:A:2816:G:C8	2.57	0.40
28:B:41:U:N3	28:B:45:G:OP2	2.53	0.40
29:a:335:C:H2'	29:a:336:A:C8	2.56	0.40
29:a:1167:G:O3'	38:j:135:LYS:HE3	2.20	0.40
29:a:1396:A:H2	29:a:1471:G:H22	1.69	0.40
39:k:66:GLU:OE2	43:o:99:ALA:HA	2.22	0.40
50:c:27:MET:SD	50:c:187:LEU:HD13	2.61	0.40
50:c:153:ASP:OD1	50:c:153:ASP:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	273/278 (98%)	265 (97%)	8 (3%)	0	100	100
2	F	212/217 (98%)	204 (96%)	7 (3%)	1 (0%)	24	57
3	G	207/215 (96%)	205 (99%)	2 (1%)	0	100	100
4	H	180/187 (96%)	173 (96%)	7 (4%)	0	100	100
5	I	163/179 (91%)	162 (99%)	1 (1%)	0	100	100
6	J	39/151 (26%)	39 (100%)	0	0	100	100
7	M	144/147 (98%)	141 (98%)	3 (2%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	131 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	Q	116/199 (58%)	114 (98%)	2 (2%)	0	100	100
11	R	124/127 (98%)	124 (100%)	0	0	100	100
12	S	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
13	T	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
14	U	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
15	V	112/153 (73%)	111 (99%)	1 (1%)	0	100	100
16	W	93/100 (93%)	92 (99%)	1 (1%)	0	100	100
17	X	89/105 (85%)	88 (99%)	1 (1%)	0	100	100
18	Z	74/88 (84%)	71 (96%)	3 (4%)	0	100	100
19	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
20	2	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
21	3	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
23	6	46/55 (84%)	42 (91%)	4 (9%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	60/64 (94%)	58 (97%)	2 (3%)	0	100	100
26	4	55/75 (73%)	54 (98%)	1 (2%)	0	100	100
30	b	148/479 (31%)	143 (97%)	5 (3%)	0	100	100
31	v	29/33 (88%)	29 (100%)	0	0	100	100
32	d	205/275 (74%)	196 (96%)	9 (4%)	0	100	100
33	e	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
34	f	166/214 (78%)	162 (98%)	4 (2%)	0	100	100
35	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
36	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
37	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
38	j	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
39	k	95/101 (94%)	90 (95%)	4 (4%)	1 (1%)	11	43
40	l	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
41	m	119/124 (96%)	112 (94%)	7 (6%)	0	100	100
42	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
43	o	98/101 (97%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	p	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
45	q	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
46	r	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
47	s	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
48	t	80/93 (86%)	77 (96%)	3 (4%)	0	100	100
49	u	83/86 (96%)	83 (100%)	0	0	100	100
50	c	226/277 (82%)	211 (93%)	15 (7%)	0	100	100
51	w	253/264 (96%)	240 (95%)	13 (5%)	0	100	100
All	All	5634/6731 (84%)	5444 (97%)	188 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	156	THR
39	k	57	LYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	215/218 (99%)	215 (100%)	0	100	100
2	F	160/163 (98%)	158 (99%)	2 (1%)	61	72
3	G	169/173 (98%)	169 (100%)	0	100	100
4	H	151/156 (97%)	150 (99%)	1 (1%)	76	78
5	I	139/150 (93%)	139 (100%)	0	100	100
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	118 (99%)	1 (1%)	73	77
8	N	100/100 (100%)	100 (100%)	0	100	100
9	O	112/114 (98%)	112 (100%)	0	100	100
10	Q	97/158 (61%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	100/100 (100%)	100 (100%)	0	100	100
13	T	97/99 (98%)	97 (100%)	0	100	100
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	90/117 (77%)	90 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	78 (99%)	1 (1%)	61	72
18	Z	55/63 (87%)	55 (100%)	0	100	100
19	1	50/51 (98%)	50 (100%)	0	100	100
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	52 (100%)	0	100	100
22	5	43/46 (94%)	43 (100%)	0	100	100
23	6	46/52 (88%)	45 (98%)	1 (2%)	45	65
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	51/63 (81%)	51 (100%)	0	100	100
30	b	132/407 (32%)	131 (99%)	1 (1%)	73	77
31	v	29/31 (94%)	29 (100%)	0	100	100
32	d	170/212 (80%)	167 (98%)	3 (2%)	51	69
33	e	175/176 (99%)	173 (99%)	2 (1%)	65	74
34	f	123/147 (84%)	123 (100%)	0	100	100
35	g	85/85 (100%)	85 (100%)	0	100	100
36	h	129/132 (98%)	129 (100%)	0	100	100
37	i	107/108 (99%)	107 (100%)	0	100	100
38	j	102/125 (82%)	102 (100%)	0	100	100
39	k	88/90 (98%)	86 (98%)	2 (2%)	44	64
40	l	89/105 (85%)	89 (100%)	0	100	100
41	m	102/105 (97%)	102 (100%)	0	100	100
42	n	99/104 (95%)	98 (99%)	1 (1%)	68	75
43	o	85/86 (99%)	83 (98%)	2 (2%)	43	64
44	p	76/77 (99%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	q	92/118 (78%)	92 (100%)	0	100	100
46	r	80/83 (96%)	78 (98%)	2 (2%)	42	63
47	s	55/72 (76%)	55 (100%)	0	100	100
48	t	73/84 (87%)	73 (100%)	0	100	100
49	u	69/70 (99%)	68 (99%)	1 (1%)	59	71
50	c	191/218 (88%)	191 (100%)	0	100	100
51	w	208/215 (97%)	207 (100%)	1 (0%)	81	80
All	All	4718/5467 (86%)	4697 (100%)	21 (0%)	81	81

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	154	CYS
2	F	156	THR
4	H	164	VAL
7	M	67	ASP
17	X	77	ASP
23	6	8	ARG
30	b	32	TYR
32	d	66	ASP
32	d	125	ASN
32	d	142	ARG
33	e	108	MET
33	e	139	ASP
39	k	8	ILE
39	k	16	GLU
42	n	56	LEU
43	o	16	LEU
43	o	48	LEU
46	r	92	GLU
46	r	94	LEU
49	u	45	ASP
51	w	131	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	87	ASN

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Mol	Chain	Res	Type
1	E	109	GLN
2	F	20	ASN
2	F	145	HIS
2	F	172	ASN
3	G	91	HIS
5	I	22	GLN
5	I	75	ASN
7	M	58	ASN
7	M	136	GLN
9	O	54	GLN
9	O	69	ASN
10	Q	61	HIS
12	S	2	ASN
12	S	28	HIS
12	S	82	HIS
13	T	27	GLN
14	U	93	GLN
20	2	40	GLN
22	5	12	ASN
23	6	20	HIS
25	8	35	HIS
26	4	6	HIS
33	e	151	GLN
33	e	173	GLN
34	f	44	ASN
34	f	146	HIS
34	f	157	ASN
37	i	16	ASN
37	i	63	GLN
38	j	47	GLN
39	k	47	ASN
40	l	31	HIS
40	l	86	HIS
41	m	105	GLN
42	n	101	GLN
45	q	17	GLN
45	q	107	ASN
49	u	7	GLN
49	u	84	ASN
50	c	36	ASN
50	c	112	GLN
51	w	35	HIS

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Mol	Chain	Res	Type
51	w	161	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3022/3119 (96%)	539 (17%)	17 (0%)
28	B	117/118 (99%)	16 (13%)	1 (0%)
29	a	1514/1528 (99%)	268 (17%)	0
All	All	4653/4765 (97%)	823 (17%)	18 (0%)

All (823) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	12	G
27	A	20	G
27	A	31	U
27	A	32	G
27	A	33	G
27	A	48	G
27	A	55	G
27	A	60	A
27	A	68	A
27	A	71	A
27	A	72	G
27	A	82	G
27	A	90	C
27	A	91	C
27	A	94	G
27	A	98	U
27	A	99	G
27	A	115	A
27	A	117	U
27	A	125	C
27	A	148	A
27	A	164	A
27	A	195	A
27	A	198	A
27	A	212	A
27	A	214	G
27	A	215	A

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Mol	Chain	Res	Type
27	A	221	A
27	A	227	A
27	A	229	U
27	A	230	G
27	A	231	U
27	A	248	G
27	A	265	A
27	A	266	U
27	A	270	U
27	A	271	A
27	A	272	A
27	A	275	C
27	A	283	U
27	A	285	U
27	A	286	G
27	A	290	C
27	A	297	G
27	A	298	G
27	A	299	G
27	A	300	G
27	A	301	U
27	A	302	U
27	A	303	G
27	A	305	G
27	A	315	U
27	A	317	G
27	A	318	U
27	A	319	G
27	A	324	C
27	A	330	U
27	A	331	U
27	A	336	C
27	A	337	U
27	A	338	C
27	A	344	G
27	A	346	C
27	A	350	A
27	A	351	G
27	A	353	G
27	A	357	U
27	A	358	G
27	A	361	A

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Mol	Chain	Res	Type
27	A	364	A
27	A	370	U
27	A	371	G
27	A	384	G
27	A	393	U
27	A	399	G
27	A	406	A
27	A	412	A
27	A	413	G
27	A	424	G
27	A	426	G
27	A	434	G
27	A	437	G
27	A	438	U
27	A	445	U
27	A	446	G
27	A	450	G
27	A	452	G
27	A	454	U
27	A	460	G
27	A	474	G
27	A	489	A
27	A	493	U
27	A	494	G
27	A	505	C
27	A	512	G
27	A	543	U
27	A	544	U
27	A	555	G
27	A	566	A
27	A	568	A
27	A	569	G
27	A	589	A
27	A	591	G
27	A	592	A
27	A	594	U
27	A	595	A
27	A	596	C
27	A	605	G
27	A	617	U
27	A	618	C
27	A	619	C

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Mol	Chain	Res	Type
27	A	620	G
27	A	635	G
27	A	636	U
27	A	637	G
27	A	638	U
27	A	639	C
27	A	640	G
27	A	642	G
27	A	644	G
27	A	655	G
27	A	664	A
27	A	667	A
27	A	679	G
27	A	684	G
27	A	685	G
27	A	696	A
27	A	706	G
27	A	707	G
27	A	708	G
27	A	709	U
27	A	721	A
27	A	731	A
27	A	738	A
27	A	740	A
27	A	754	C
27	A	756	A
27	A	758	A
27	A	760	U
27	A	764	U
27	A	765	G
27	A	766	G
27	A	768	G
27	A	784	G
27	A	785	A
27	A	801	U
27	A	832	G
27	A	839	U
27	A	841	G
27	A	845	C
27	A	862	U
27	A	863	G
27	A	868	C

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Mol	Chain	Res	Type
27	A	872	G
27	A	878	G
27	A	879	A
27	A	880	G
27	A	890	G
27	A	891	G
27	A	897	A
27	A	899	G
27	A	907	A
27	A	920	G
27	A	927	C
27	A	942	U
27	A	945	G
27	A	960	G
27	A	961	U
27	A	972	A
27	A	975	U
27	A	981	U
27	A	982	A
27	A	988	U
27	A	989	G
27	A	990	G
27	A	991	C
27	A	994	A
27	A	995	U
27	A	1001	C
27	A	1002	C
27	A	1003	A
27	A	1004	C
27	A	1005	A
27	A	1008	G
27	A	1009	U
27	A	1010	U
27	A	1012	C
27	A	1013	U
27	A	1014	G
27	A	1015	A
27	A	1018	U
27	A	1019	C
27	A	1022	C
27	A	1025	A
27	A	1030	C

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Mol	Chain	Res	Type
27	A	1047	A
27	A	1049	G
27	A	1058	A
27	A	1063	G
27	A	1076	A
27	A	1078	G
27	A	1085	G
27	A	1092	G
27	A	1101	A
27	A	1114	G
27	A	1130	C
27	A	1131	G
27	A	1138	A
27	A	1144	A
27	A	1151	U
27	A	1158	U
27	A	1164	A
27	A	1230	G
27	A	1232	G
27	A	1235	U
27	A	1238	G
27	A	1240	G
27	A	1242	C
27	A	1244	A
27	A	1245	U
27	A	1248	U
27	A	1250	U
27	A	1251	A
27	A	1252	G
27	A	1253	C
27	A	1260	C
27	A	1261	A
27	A	1292	U
27	A	1293	G
27	A	1298	C
27	A	1335	G
27	A	1344	A
27	A	1351	G
27	A	1353	G
27	A	1359	G
27	A	1362	A
27	A	1371	G

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Mol	Chain	Res	Type
27	A	1386	G
27	A	1387	A
27	A	1389	U
27	A	1415	A
27	A	1416	A
27	A	1436	C
27	A	1440	C
27	A	1456	G
27	A	1465	C
27	A	1467	U
27	A	1480	A
27	A	1493	A
27	A	1494	U
27	A	1499	A
27	A	1507	G
27	A	1508	A
27	A	1510	A
27	A	1511	U
27	A	1522	G
27	A	1531	C
27	A	1533	U
27	A	1534	C
27	A	1539	A
27	A	1540	U
27	A	1543	A
27	A	1550	G
27	A	1551	U
27	A	1552	A
27	A	1553	C
27	A	1554	U
27	A	1562	C
27	A	1563	A
27	A	1609	G
27	A	1611	A
27	A	1625	G
27	A	1627	U
27	A	1628	A
27	A	1629	G
27	A	1630	U
27	A	1633	U
27	A	1639	G
27	A	1640	A

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Mol	Chain	Res	Type
27	A	1641	U
27	A	1648	A
27	A	1649	C
27	A	1670	G
27	A	1676	G
27	A	1679	A
27	A	1680	A
27	A	1681	U
27	A	1703	G
27	A	1710	A
27	A	1711	G
27	A	1714	A
27	A	1717	U
27	A	1724	G
27	A	1728	U
27	A	1731	A
27	A	1737	A
27	A	1754	G
27	A	1755	A
27	A	1756	G
27	A	1757	U
27	A	1767	U
27	A	1786	G
27	A	1789	A
27	A	1798	U
27	A	1826	A
27	A	1864	U
27	A	1866	C
27	A	1871	G
27	A	1872	A
27	A	1892	G
27	A	1933	G
27	A	1946	U
27	A	1947	U
27	A	1949	C
27	A	1950	G
27	A	1973	C
27	A	1975	A
27	A	1981	U
27	A	1990	A
27	A	2003	A
27	A	2017	C

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Mol	Chain	Res	Type
27	A	2018	G
27	A	2026	A
27	A	2033	U
27	A	2046	A
27	A	2064	A
27	A	2065	A
27	A	2074	G
27	A	2075	G
27	A	2085	C
27	A	2086	U
27	A	2087	C
27	A	2088	C
27	A	2089	C
27	A	2091	U
27	A	2092	U
27	A	2093	G
27	A	2094	G
27	A	2095	G
27	A	2096	G
27	A	2107	G
27	A	2130	G
27	A	2137	A
27	A	2141	U
27	A	2153	G
27	A	2154	G
27	A	2160	A
27	A	2161	A
27	A	2162	A
27	A	2163	U
27	A	2179	U
27	A	2191	C
27	A	2194	A
27	A	2195	U
27	A	2196	G
27	A	2215	U
27	A	2217	U
27	A	2221	A
27	A	2244	A
27	A	2247	A
27	A	2251	G
27	A	2254	A
27	A	2255	A

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Mol	Chain	Res	Type
27	A	2256	G
27	A	2257	A
27	A	2263	G
27	A	2267	C
27	A	2276	G
27	A	2279	C
27	A	2280	G
27	A	2283	A
27	A	2284	A
27	A	2285	G
27	A	2286	A
27	A	2287	C
27	A	2316	G
27	A	2320	C
27	A	2322	C
27	A	2324	A
27	A	2325	U
27	A	2328	G
27	A	2330	U
27	A	2331	U
27	A	2334	U
27	A	2335	G
27	A	2338	G
27	A	2339	G
27	A	2340	A
27	A	2341	U
27	A	2342	A
27	A	2343	G
27	A	2345	U
27	A	2346	G
27	A	2351	A
27	A	2353	U
27	A	2354	G
27	A	2355	U
27	A	2356	G
27	A	2357	A
27	A	2368	C
27	A	2370	A
27	A	2371	G
27	A	2372	U
27	A	2382	G
27	A	2384	C

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Mol	Chain	Res	Type
27	A	2386	U
27	A	2387	U
27	A	2388	G
27	A	2390	U
27	A	2393	A
27	A	2394	A
27	A	2395	U
27	A	2396	A
27	A	2399	A
27	A	2401	U
27	A	2402	C
27	A	2403	U
27	A	2404	G
27	A	2405	A
27	A	2407	C
27	A	2408	G
27	A	2410	A
27	A	2413	G
27	A	2421	A
27	A	2422	A
27	A	2427	G
27	A	2434	A
27	A	2436	A
27	A	2447	G
27	A	2449	A
27	A	2462	G
27	A	2463	G
27	A	2467	U
27	A	2503	G
27	A	2507	C
27	A	2511	A
27	A	2512	A
27	A	2529	A
27	A	2532	G
27	A	2544	U
27	A	2545	G
27	A	2548	U
27	A	2549	G
27	A	2558	C
27	A	2559	A
27	A	2560	A
27	A	2569	G

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Mol	Chain	Res	Type
27	A	2571	C
27	A	2574	C
27	A	2585	U
27	A	2607	G
27	A	2609	A
27	A	2626	U
27	A	2627	C
27	A	2647	U
27	A	2649	A
27	A	2653	G
27	A	2654	A
27	A	2655	U
27	A	2659	A
27	A	2665	C
27	A	2671	G
27	A	2672	A
27	A	2673	U
27	A	2677	A
27	A	2678	G
27	A	2679	G
27	A	2688	C
27	A	2693	A
27	A	2694	G
27	A	2700	A
27	A	2705	G
27	A	2714	G
27	A	2715	U
27	A	2718	G
27	A	2722	C
27	A	2726	G
27	A	2727	A
27	A	2729	G
27	A	2730	U
27	A	2737	G
27	A	2742	A
27	A	2744	C
27	A	2749	G
27	A	2753	G
27	A	2754	G
27	A	2756	G
27	A	2759	G
27	A	2766	A

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Mol	Chain	Res	Type
27	A	2786	U
27	A	2790	A
27	A	2791	G
27	A	2796	A
27	A	2797	C
27	A	2800	G
27	A	2801	A
27	A	2826	A
27	A	2827	G
27	A	2833	U
27	A	2837	U
27	A	2839	U
27	A	2853	C
27	A	2854	A
27	A	2857	A
27	A	2858	G
27	A	2862	G
27	A	2876	C
27	A	2913	U
27	A	2915	C
27	A	2926	A
27	A	2936	C
27	A	2938	G
27	A	2950	C
27	A	2956	G
27	A	2957	A
27	A	2968	G
27	A	2980	U
27	A	2981	A
27	A	2982	A
27	A	2985	G
27	A	2989	A
27	A	3002	A
27	A	3009	U
27	A	3014	A
27	A	3021	A
27	A	3022	G
27	A	3029	U
27	A	3042	A
27	A	3044	A
27	A	3056	A
27	A	3082	U

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Mol	Chain	Res	Type
27	A	3088	C
27	A	3093	A
27	A	3105	C
27	A	3106	C
27	A	3107	G
27	A	3108	G
27	A	3114	A
28	B	3	U
28	B	4	A
28	B	9	G
28	B	11	U
28	B	12	C
28	B	13	C
28	B	27	A
28	B	30	G
28	B	36	U
28	B	42	C
28	B	54	A
28	B	57	U
28	B	68	G
28	B	87	U
28	B	89	C
28	B	107	A
29	a	12	A
29	a	13	G
29	a	36	A
29	a	43	G
29	a	51	C
29	a	52	U
29	a	55	A
29	a	58	C
29	a	59	A
29	a	74	A
29	a	82	U
29	a	86	G
29	a	87	G
29	a	93	C
29	a	116	A
29	a	117	C
29	a	126	G
29	a	128	U
29	a	146	A

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Mol	Chain	Res	Type
29	a	160	C
29	a	192	G
29	a	193	C
29	a	200	U
29	a	210	A
29	a	211	A
29	a	216	U
29	a	217	U
29	a	220	G
29	a	231	G
29	a	243	A
29	a	245	C
29	a	247	G
29	a	251	G
29	a	252	U
29	a	266	G
29	a	267	C
29	a	279	A
29	a	280	C
29	a	281	G
29	a	289	G
29	a	329	A
29	a	330	C
29	a	332	G
29	a	344	A
29	a	345	C
29	a	347	G
29	a	351	G
29	a	352	C
29	a	353	A
29	a	354	G
29	a	367	U
29	a	372	C
29	a	373	A
29	a	390	U
29	a	392	C
29	a	397	A
29	a	398	C
29	a	406	G
29	a	414	A
29	a	421	U
29	a	422	C

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Mol	Chain	Res	Type
29	a	423	G
29	a	424	G
29	a	426	U
29	a	428	G
29	a	429	U
29	a	430	A
29	a	433	C
29	a	434	C
29	a	452	A
29	a	453	G
29	a	456	C
29	a	457	A
29	a	458	A
29	a	459	G
29	a	461	G
29	a	465	G
29	a	466	U
29	a	475	A
29	a	476	A
29	a	477	G
29	a	478	A
29	a	485	G
29	a	486	G
29	a	491	C
29	a	497	G
29	a	498	C
29	a	499	C
29	a	501	G
29	a	507	G
29	a	509	G
29	a	511	U
29	a	512	A
29	a	513	A
29	a	515	A
29	a	519	A
29	a	520	G
29	a	527	A
29	a	539	A
29	a	542	U
29	a	544	C
29	a	552	A
29	a	553	A

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Mol	Chain	Res	Type
29	a	556	A
29	a	557	G
29	a	576	C
29	a	612	U
29	a	613	G
29	a	629	G
29	a	633	A
29	a	645	G
29	a	666	U
29	a	668	G
29	a	683	G
29	a	701	G
29	a	702	G
29	a	703	U
29	a	711	G
29	a	729	A
29	a	735	G
29	a	761	A
29	a	765	G
29	a	772	A
29	a	773	U
29	a	774	A
29	a	789	G
29	a	793	U
29	a	794	A
29	a	795	A
29	a	796	A
29	a	797	C
29	a	808	A
29	a	818	U
29	a	821	C
29	a	822	U
29	a	823	U
29	a	824	C
29	a	826	U
29	a	827	U
29	a	828	G
29	a	829	G
29	a	841	U
29	a	871	A
29	a	884	G
29	a	896	A

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Mol	Chain	Res	Type
29	a	908	G
29	a	909	G
29	a	913	C
29	a	914	C
29	a	916	C
29	a	917	A
29	a	942	U
29	a	943	U
29	a	950	A
29	a	951	A
29	a	953	G
29	a	956	A
29	a	957	A
29	a	958	G
29	a	959	A
29	a	973	U
29	a	974	U
29	a	975	G
29	a	976	A
29	a	981	C
29	a	982	A
29	a	988	C
29	a	990	C
29	a	1007	U
29	a	1008	C
29	a	1011	U
29	a	1012	U
29	a	1013	G
29	a	1014	U
29	a	1017	C
29	a	1020	G
29	a	1021	U
29	a	1022	G
29	a	1025	C
29	a	1033	G
29	a	1034	C
29	a	1036	U
29	a	1045	U
29	a	1074	G
29	a	1075	U
29	a	1081	A
29	a	1088	G

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Mol	Chain	Res	Type
29	a	1104	G
29	a	1108	C
29	a	1110	A
29	a	1115	G
29	a	1116	U
29	a	1117	U
29	a	1118	A
29	a	1119	U
29	a	1120	G
29	a	1138	A
29	a	1140	U
29	a	1147	G
29	a	1148	U
29	a	1149	C
29	a	1150	A
29	a	1151	A
29	a	1162	G
29	a	1164	U
29	a	1165	G
29	a	1171	G
29	a	1176	C
29	a	1177	A
29	a	1178	A
29	a	1181	C
29	a	1182	A
29	a	1193	U
29	a	1194	A
29	a	1195	U
29	a	1217	A
29	a	1231	A
29	a	1237	C
29	a	1238	U
29	a	1241	G
29	a	1249	G
29	a	1251	G
29	a	1261	A
29	a	1266	U
29	a	1267	U
29	a	1268	C
29	a	1283	U
29	a	1284	U
29	a	1285	C

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Mol	Chain	Res	Type
29	a	1287	G
29	a	1302	C
29	a	1328	A
29	a	1329	G
29	a	1342	A
29	a	1343	G
29	a	1344	C
29	a	1345	A
29	a	1346	A
29	a	1347	C
29	a	1353	G
29	a	1357	A
29	a	1364	U
29	a	1381	A
29	a	1405	G
29	a	1424	G
29	a	1425	G
29	a	1426	C
29	a	1429	A
29	a	1433	C
29	a	1434	U
29	a	1435	U
29	a	1436	G
29	a	1438	G
29	a	1440	A
29	a	1463	G
29	a	1476	A
29	a	1481	G
29	a	1483	A
29	a	1488	G
29	a	1490	U
29	a	1501	G
29	a	1503	A
29	a	1504	G
29	a	1513	G
29	a	1514	G
29	a	1517	C
29	a	1518	A
29	a	1522	C

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	89	A
27	A	97	U
27	A	316	U
27	A	357	U
27	A	445	U
27	A	641	U
27	A	643	G
27	A	974	G
27	A	1002	C
27	A	1004	C
27	A	1084	U
27	A	1117	U
27	A	1561	C
27	A	2094	G
27	A	2350	G
27	A	2381	A
27	A	2729	G
28	B	10	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

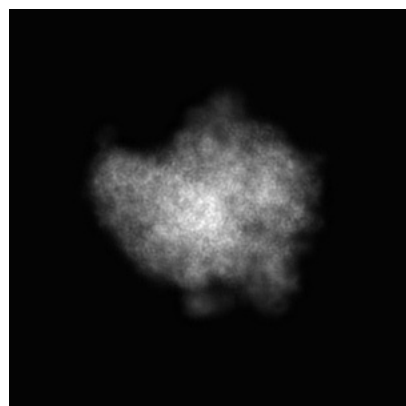
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37559. These allow visual inspection of the internal detail of the map and identification of artifacts.

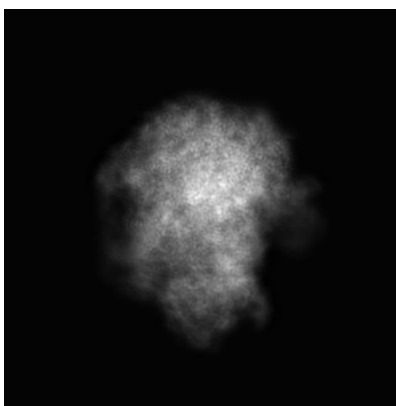
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

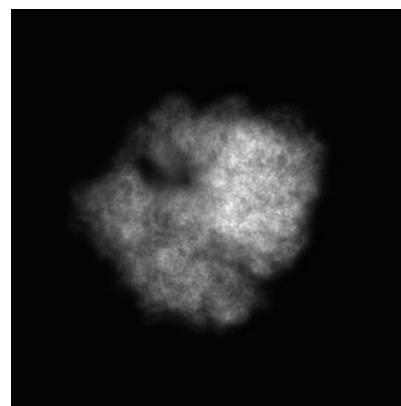
6.1.1 Primary map



X

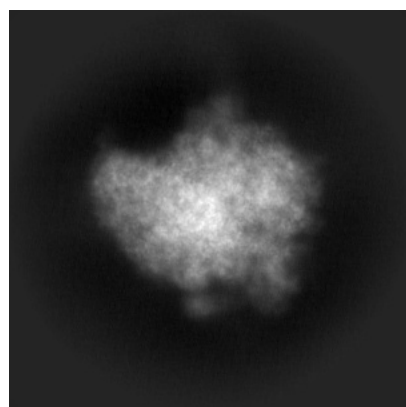


Y

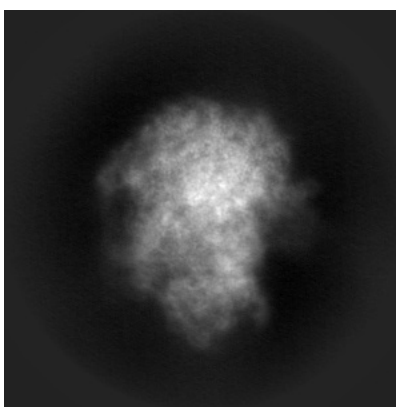


Z

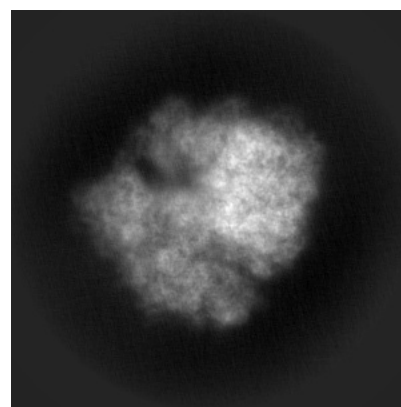
6.1.2 Raw map



X



Y

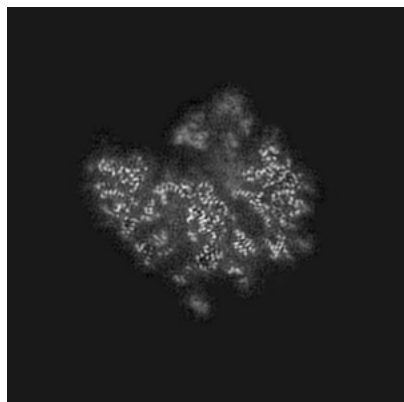


Z

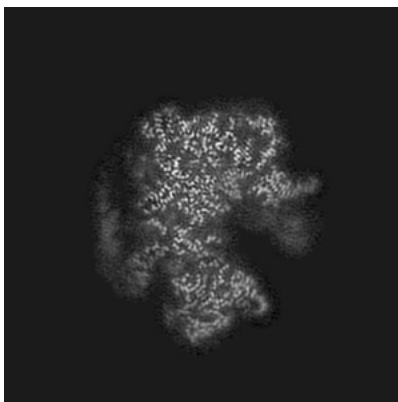
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

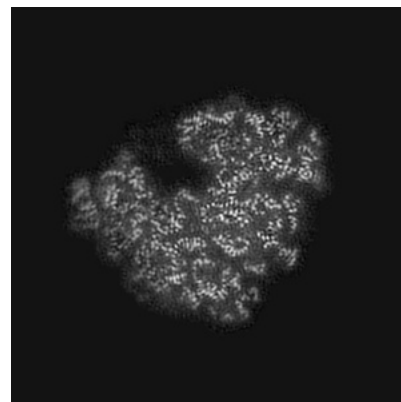
6.2.1 Primary map



X Index: 190

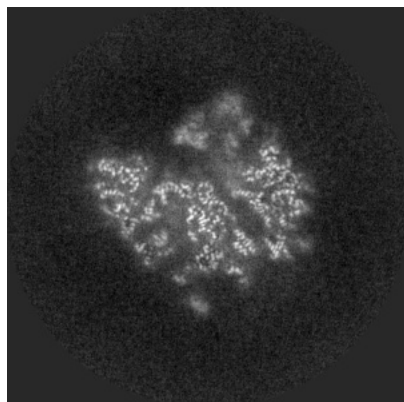


Y Index: 190

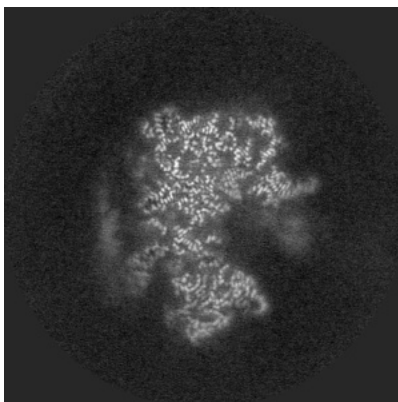


Z Index: 190

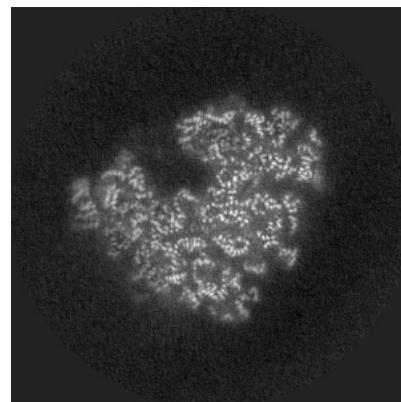
6.2.2 Raw map



X Index: 190



Y Index: 190

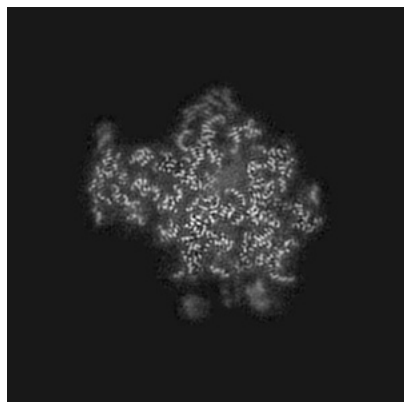


Z Index: 190

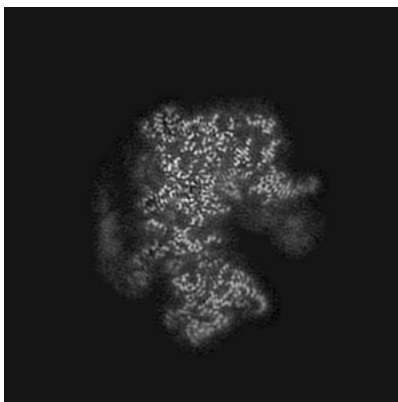
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

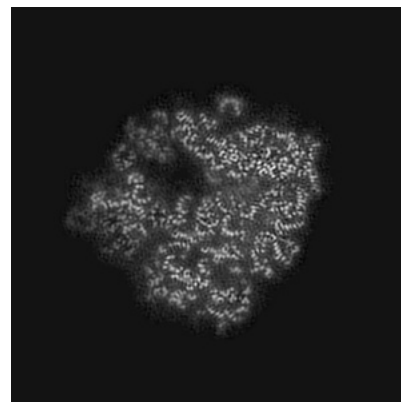
6.3.1 Primary map



X Index: 210

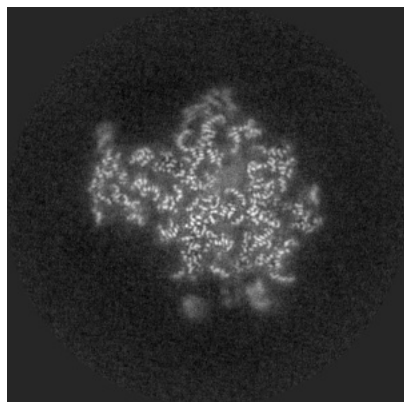


Y Index: 191

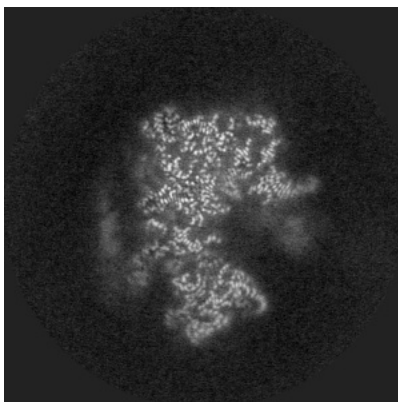


Z Index: 200

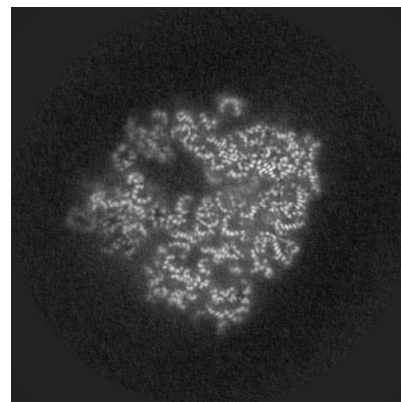
6.3.2 Raw map



X Index: 210



Y Index: 191

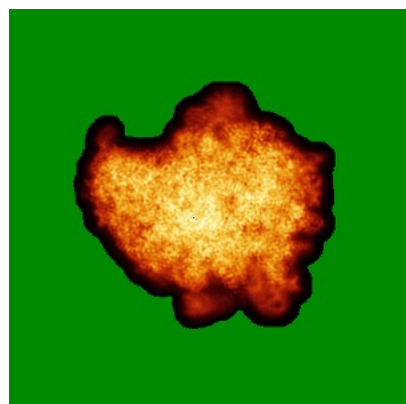


Z Index: 200

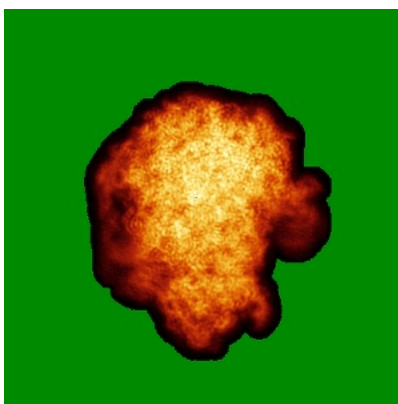
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

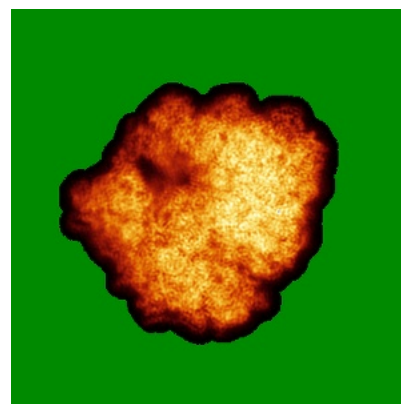
6.4.1 Primary map



X

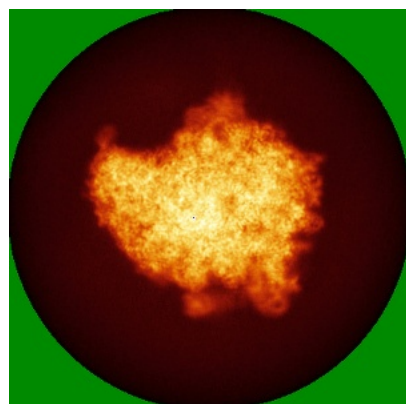


Y

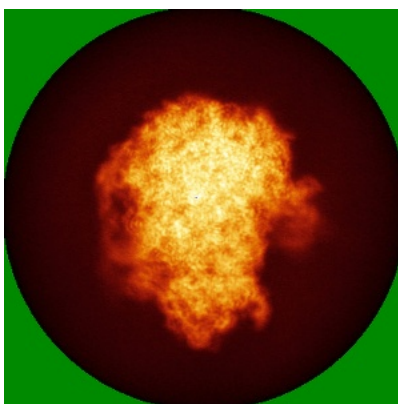


Z

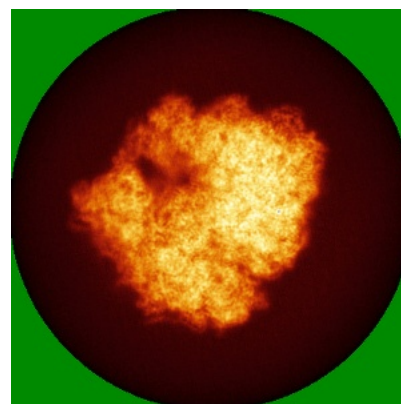
6.4.2 Raw map



X



Y

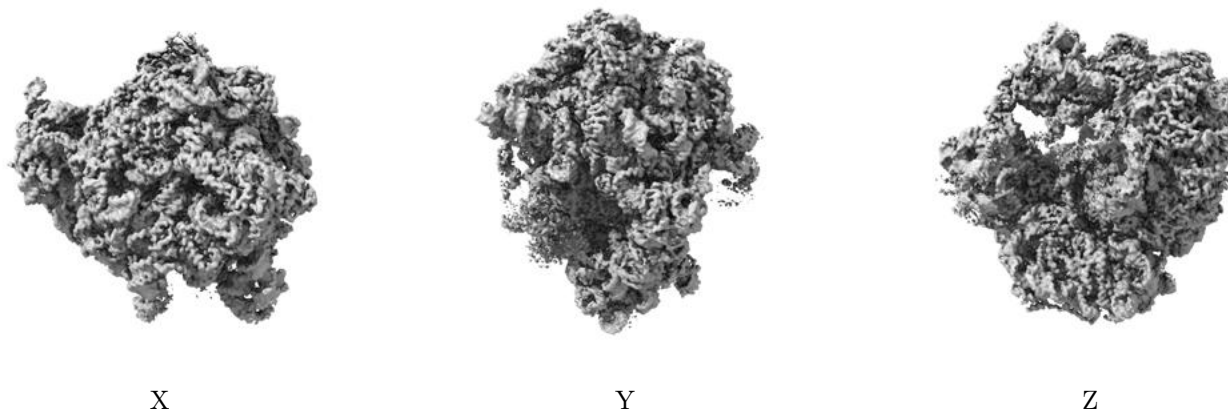


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

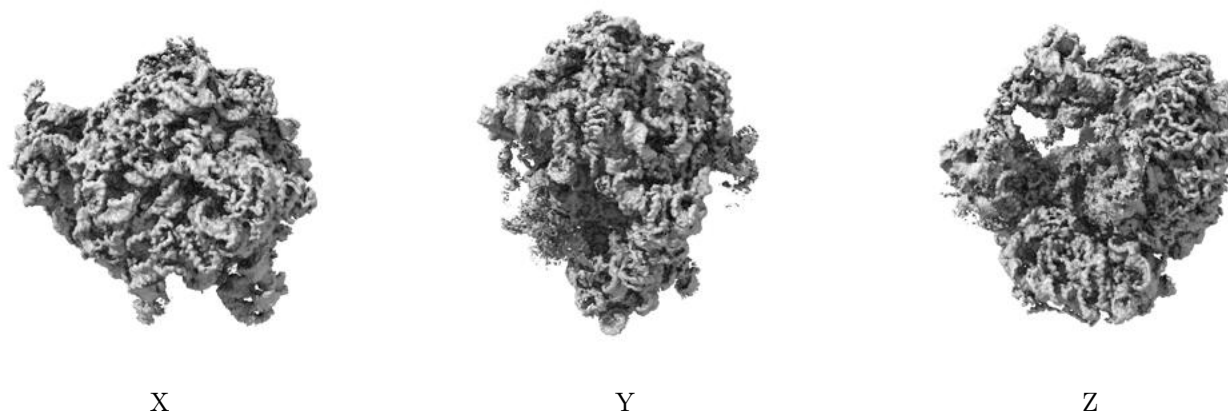
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

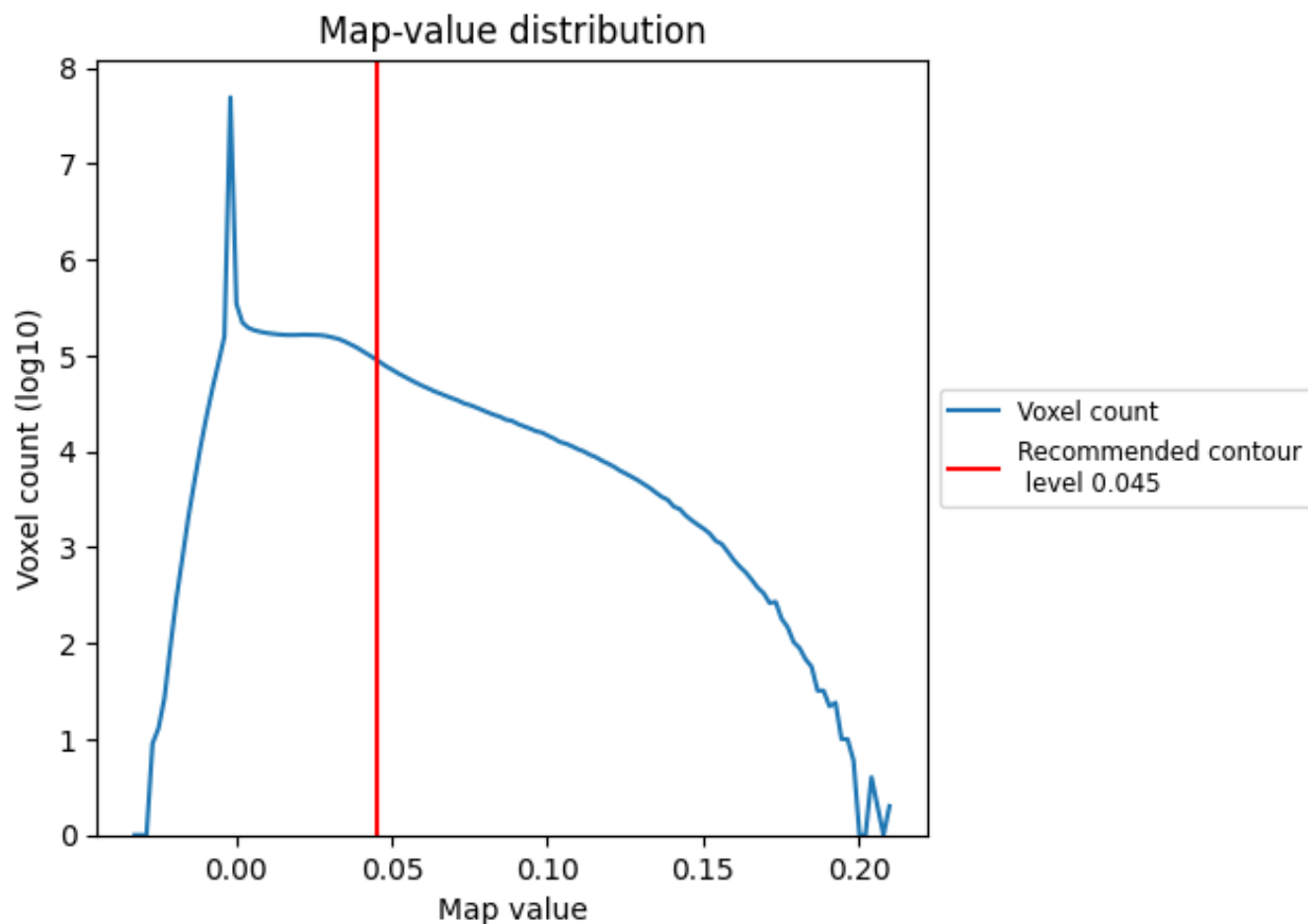
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

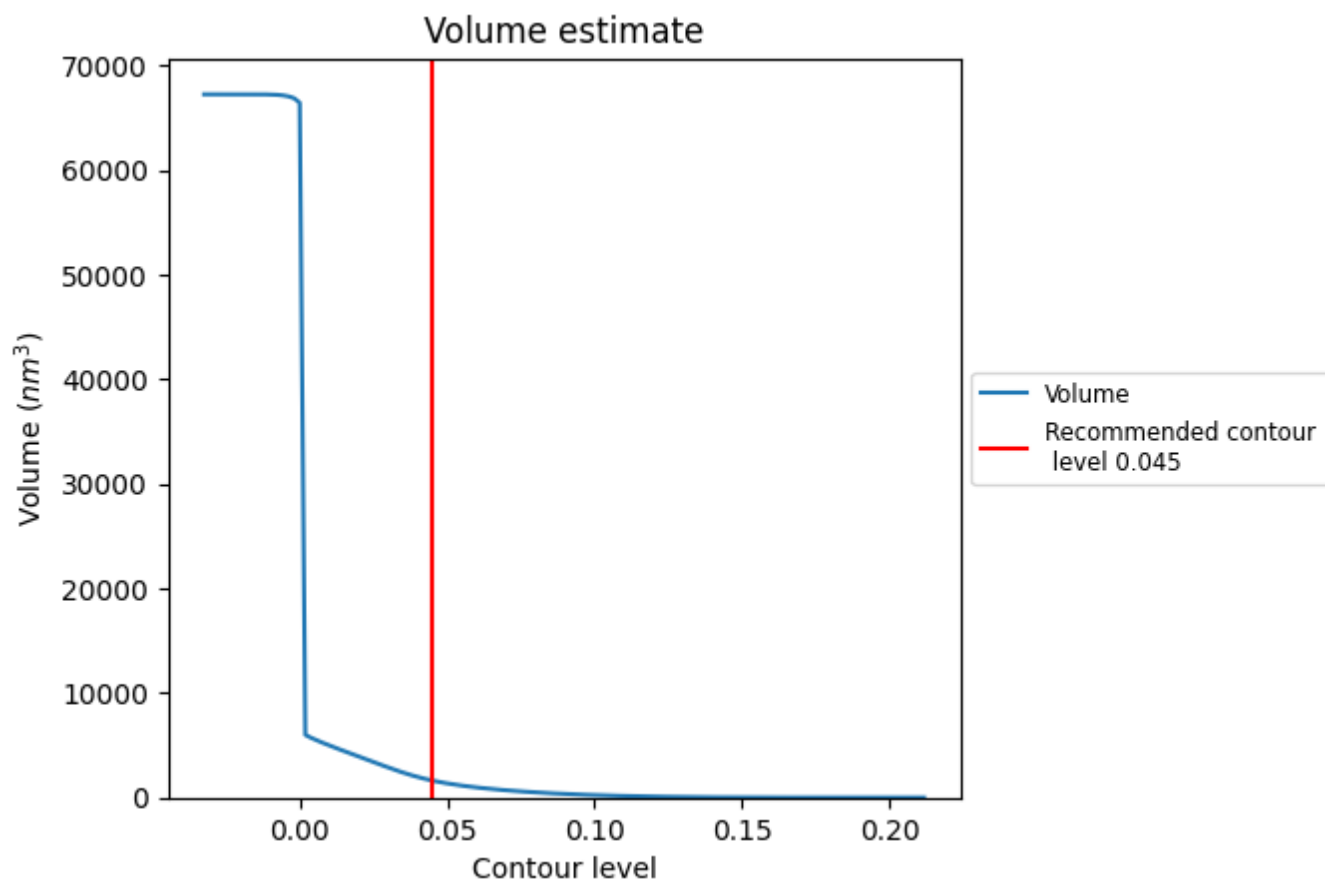
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

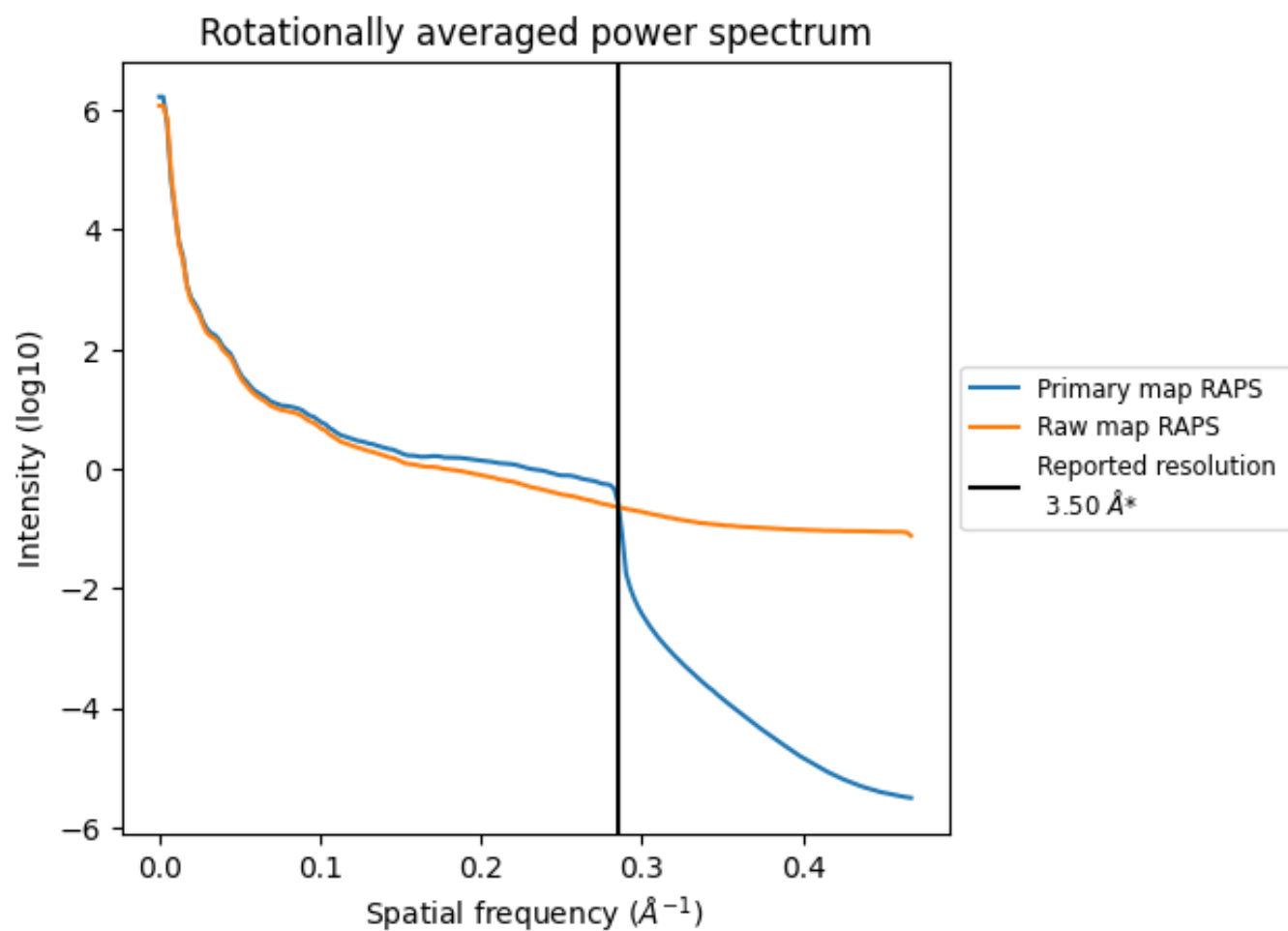
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1622 nm³; this corresponds to an approximate mass of 1465 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

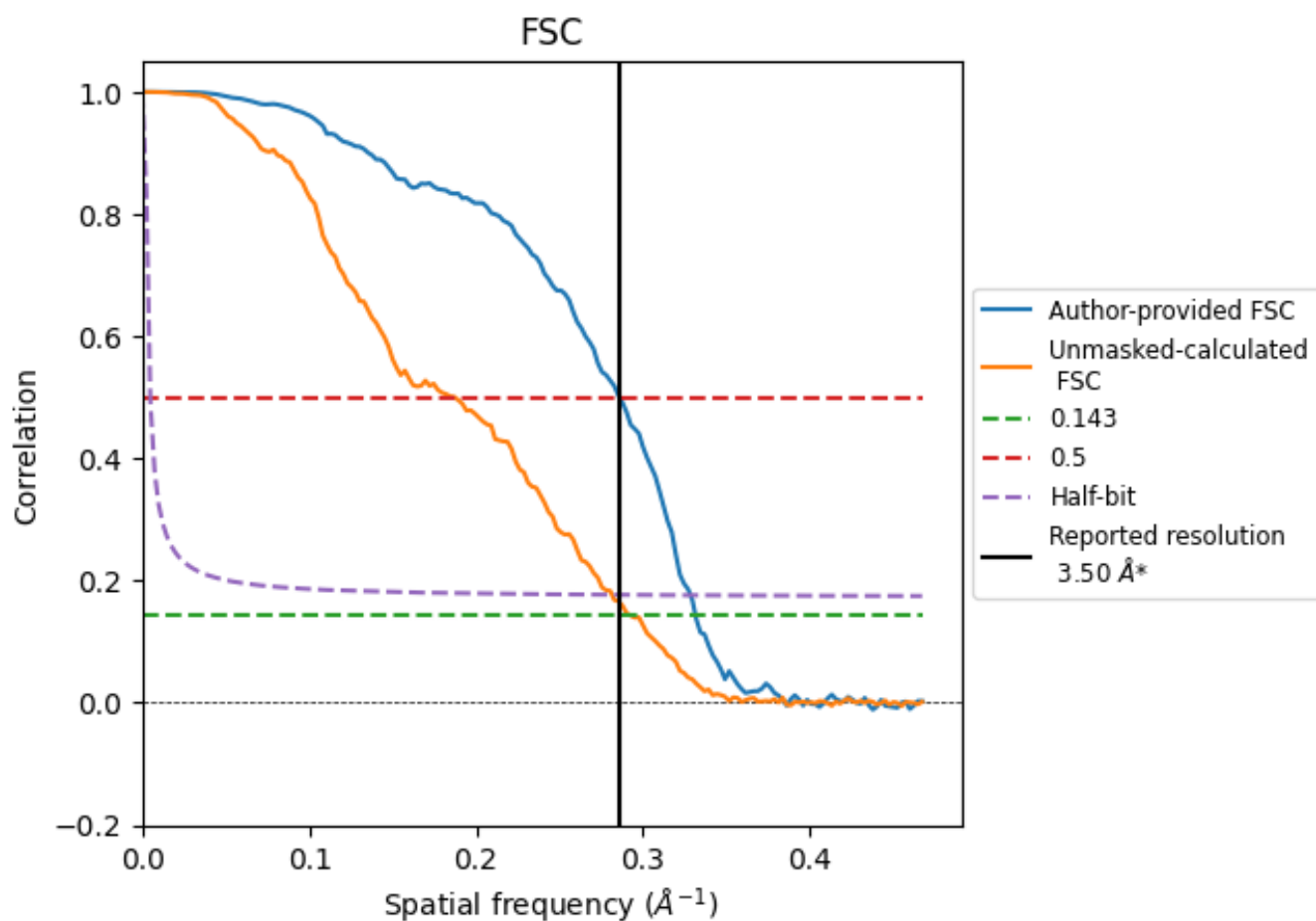


*Reported resolution corresponds to spatial frequency of $0.286 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

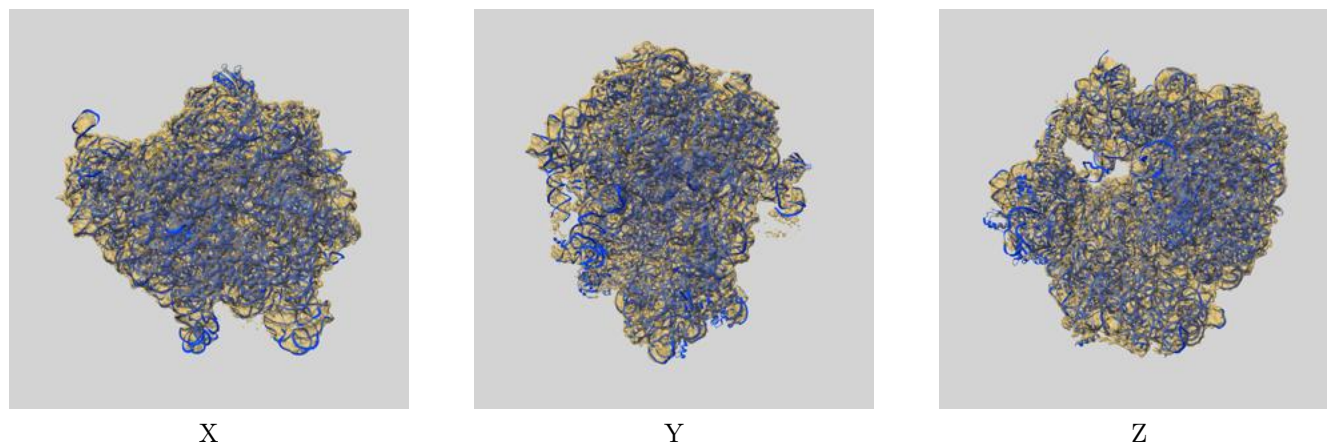
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.02	3.50	3.04
Unmasked-calculated*	3.42	5.34	3.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.02 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

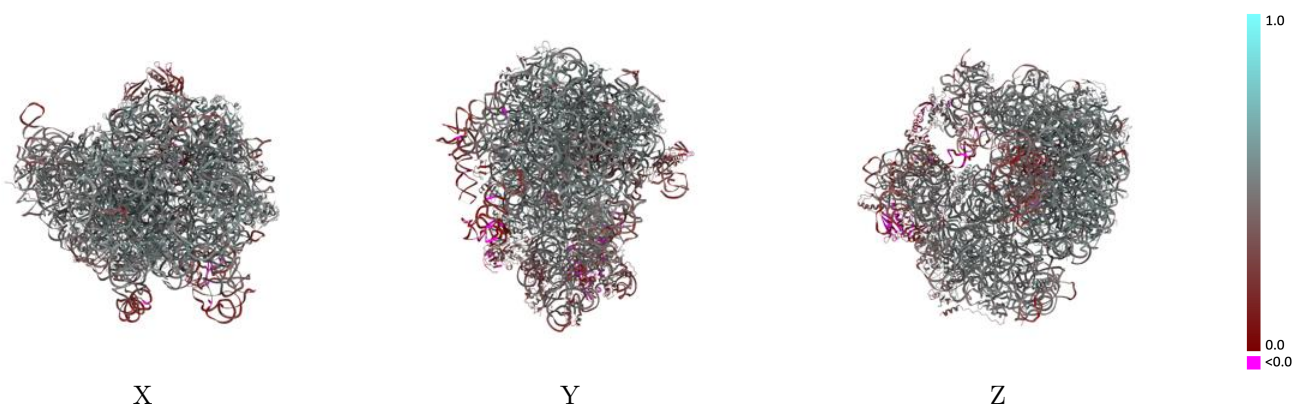
This section contains information regarding the fit between EMDB map EMD-37559 and PDB model 8WI7. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



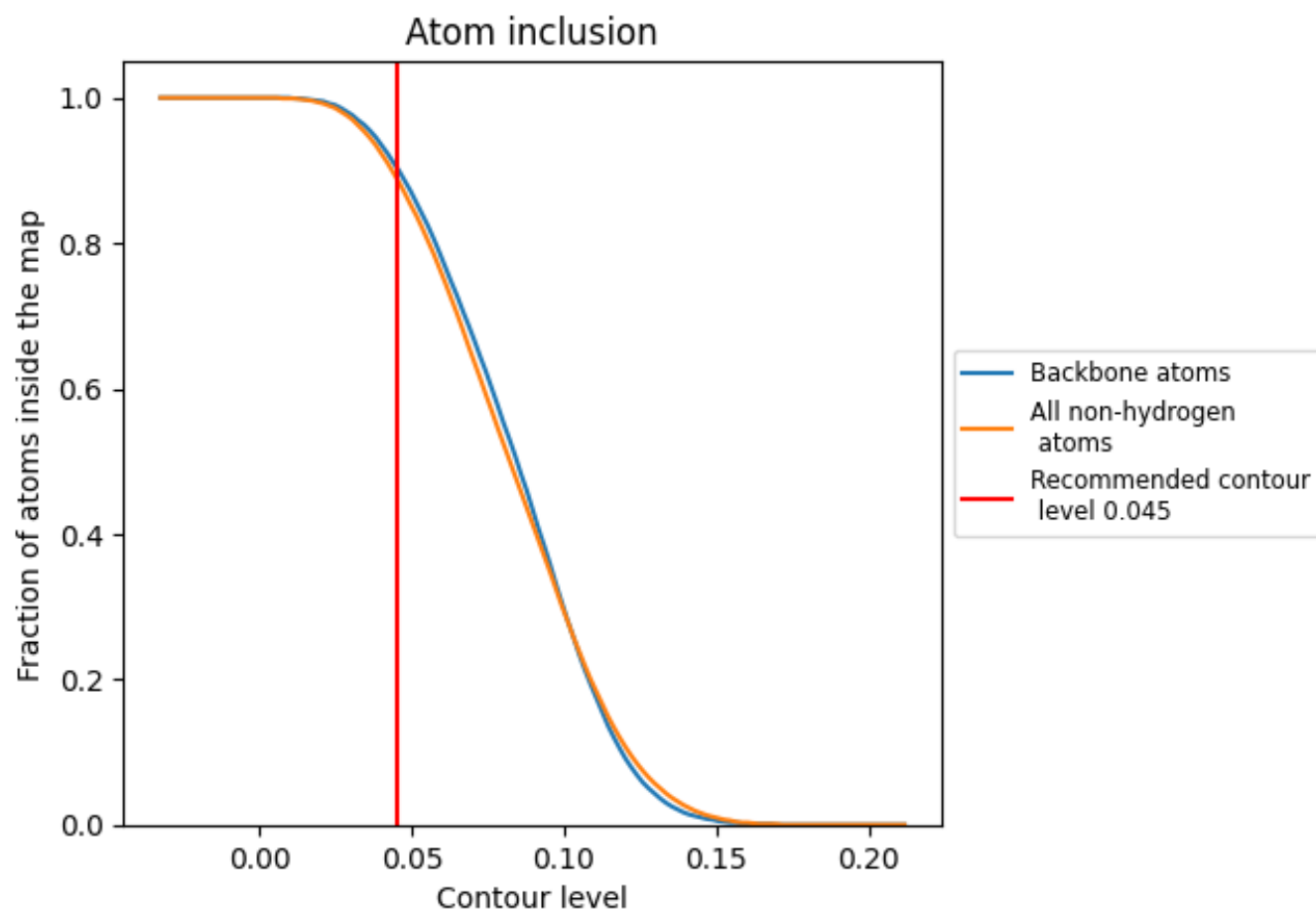
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.4480
1	 0.8870	 0.4740
2	 0.8290	 0.4720
3	 0.8870	 0.5080
4	 0.3240	 0.1470
5	 0.8530	 0.5140
6	 0.5620	 0.2770
7	 0.9940	 0.4920
8	 0.8930	 0.5180
A	 0.9260	 0.4580
B	 0.9440	 0.4300
E	 0.9670	 0.5360
F	 0.9220	 0.5300
G	 0.8930	 0.5060
H	 0.7810	 0.4110
I	 0.4780	 0.2610
J	 0.5430	 0.2690
M	 0.9280	 0.5110
N	 0.9360	 0.5230
O	 0.8900	 0.5000
Q	 0.9610	 0.5370
R	 0.8100	 0.4400
S	 0.8970	 0.4870
T	 0.9340	 0.5160
U	 0.8860	 0.5350
V	 0.9680	 0.5370
W	 0.8960	 0.5170
X	 0.8200	 0.4780
Z	 0.9450	 0.5260
a	 0.9630	 0.4570
b	 0.2710	 0.2050
c	 0.6970	 0.3630
d	 0.2170	 0.0800
e	 0.8310	 0.4530
f	 0.8400	 0.4590



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Chain	Atom inclusion	Q-score
g	 0.8130	 0.4670
h	 0.7130	 0.3330
i	 0.9200	 0.5010
j	 0.7630	 0.3970
k	 0.5080	 0.4090
l	 0.8630	 0.4680
m	 0.8930	 0.4950
n	 0.6820	 0.2270
o	 0.4980	 0.3780
p	 0.8760	 0.4820
q	 0.8450	 0.4760
r	 0.8790	 0.4500
s	 0.8080	 0.4180
t	 0.6910	 0.3250
u	 0.8840	 0.4770
v	 0.9680	 0.4840
w	 0.6440	 0.3880